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OM protein - protein search, using sw model

Run on: July 26, 2005, 23:47:55 ; Search time 164 Seconds  
(without alignments)  
11.791 Million cell updates/sec

Title: US-10-632-678-10

Perfect score: 34

Sequence: 1 CHAVC 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 396760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A Geneseq\_16Dec04:\*

- 1: geneseqp1990s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	5	2	AAW23979 Cadherin-
2	34	100.0	5	2	AAW91033 Peptide i
3	34	100.0	5	2	AAW91021 Peptide i
4	34	100.0	5	2	AAW17108 Cadherin-
5	34	100.0	5	3	AAW27334 Beta-cate
6	34	100.0	5	3	AAW27346 Beta-cate
7	34	100.0	5	3	AAW73790 N-cadheri
8	34	100.0	5	4	AAW65370 Cyclic pe
9	34	100.0	5	5	AAW47477 Cyclic pe
10	34	100.0	5	6	ABU60211 N-cadheri
11	34	100.0	5	7	ABO43539 Classical
12	34	100.0	5	8	ADK13544 Cadherin-
13	34	100.0	6	4	AAW65445 Cyclic pe
14	34	100.0	6	4	AAW65449 Cyclic pe
15	34	100.0	6	4	AAW65441 Cyclic pe
16	34	100.0	6	4	AAW65444 Cyclic pe
17	34	100.0	6	4	AAW65450 Cyclic pe
18	34	100.0	6	4	AAW65448 Cyclic pe
19	34	100.0	6	5	AAW47551 Peptide,
20	34	100.0	6	5	AAW47521 Cyclic pe
21	34	100.0	6	5	AAW47555 Cyclic pe
22	34	100.0	6	5	AAW47554 Cyclic pe
23	34	100.0	6	5	AAW47558 Cyclic pe
24	34	100.0	6	5	AAW47560 Cyclic pe
25	34	100.0	6	5	AAW47559 Cyclic pe

26	34	100.0	6	7	ABO43613 Classical
27	34	100.0	6	7	ABO43610 Classical
28	34	100.0	6	7	ABO43617 Classical
29	34	100.0	6	7	ABO43618 Classical
30	34	100.0	6	7	ABO43614 Classical
31	34	100.0	6	7	ABO43619 Classical
32	34	100.0	6	8	ADK13619 Cadherin-
33	34	100.0	6	8	ADK13622 Cadherin-
34	34	100.0	6	8	ADK13623 Cadherin-
35	34	100.0	6	8	ADK13615 Cadherin-
36	34	100.0	6	8	ADK13624 Cadherin-
37	34	100.0	6	8	ADK13618 Cadherin-
38	34	100.0	7	4	AAW65447 Cyclic pe
39	34	100.0	7	4	AAW65446 Cyclic pe
40	34	100.0	7	5	AAW47556 Cyclic pe
41	34	100.0	7	5	AAW47563 Cyclic pe
42	34	100.0	7	5	AAW47557 Cyclic pe
43	34	100.0	7	7	ABO43616 Classical
44	34	100.0	7	7	ABO43615 Classical
45	34	100.0	7	8	ADK13620 Cadherin-
46	34	100.0	7	8	ADK13621 Cadherin-
47	34	100.0	8	5	AAW47562 Cyclic pe
48	34	100.0	61	3	AAW68110 Kunitz pr
49	34	100.0	61	3	AAW68085 Kunitz pr
50	34	100.0	121	4	AAU28273 Novel hum
51	34	100.0	198	3	AAW38298 Arabidops
52	34	100.0	198	3	AAW07319 Arabidops
53	34	100.0	244	3	AAW38297 Arabidops
54	34	100.0	244	3	AAW07318 Arabidops
55	34	100.0	380	4	ABW67444 Drosophil
56	34	100.0	381	5	ABW83912 Drosophil
57	34	100.0	537	7	ADW97396 Porcine i
58	34	100.0	542	7	ADW74464 Mycobacte
59	33	97.1	75	8	ADK16783 Nancarcha
60	33	97.1	176	4	AAU50581 Propionib
61	33	97.1	176	6	ABW47100 Propionib
62	33	97.1	428	5	ABW92762 Herbicida
63	33	97.1	672	4	AAW72708 Parvoviru
64	33	97.1	672	4	AAW72710 Parvoviru
65	33	97.1	672	4	AAW72706 Parvoviru
66	33	97.1	672	4	AAW72702 Parvoviru
67	33	97.1	672	4	AAW72704 Parvoviru
68	31	91.2	16	8	ADO34065 Human CLA
69	31	91.2	20	4	AAW15812 Peptide #
70	31	91.2	20	4	ABW34809 Peptide #
71	31	91.2	20	4	AAW28322 Peptide #
72	31	91.2	20	4	ABW29631 Peptide #
73	31	91.2	20	4	ABW20225 Protein #
74	31	91.2	20	4	AAW67996 Human bon
75	31	91.2	20	4	AAW55611 Human bra
76	31	91.2	20	4	ABW49637 Human liv
77	31	91.2	20	4	AAW03550 Peptide #
78	31	91.2	20	5	ABW37528 Human pep
79	31	91.2	53	5	ABW07522 Human ORF
80	31	91.2	58	4	ABW08832 Novel hum
81	31	91.2	61	4	AAW09658 Human pol
82	31	91.2	63	2	AAW27620 Human sec
83	31	91.2	63	4	AAW15142 Peptide #
84	31	91.2	63	4	ABW34134 Peptide #
85	31	91.2	63	4	AAW27597 Peptide #
86	31	91.2	63	4	ABW28966 Peptide #
87	31	91.2	63	4	ABW19575 Protein #
88	31	91.2	63	4	AAW67305 Human bon
89	31	91.2	63	4	AAW54924 Human bra
90	31	91.2	63	4	ABW48967 Human liv
91	31	91.2	63	4	AAW02883 Peptide #
92	31	91.2	63	5	ABW36952 Human pep
93	31	91.2	85	4	AAW24070 Human EST
94	31	91.2	96	4	AAU14419 Human nov
95	31	91.2	96	8	ADW80737 Human pol
96	31	91.2	100	8	ADO34044 Human CLA
97	31	91.2	117	7	ADW05223 Human pro
98	31	91.2	134	4	ABW05990 Novel hum

99 31 91.2 139 7 ADM26297 Adm26297 Hyperther  
100 31 91.2 148 6 ABJ18656 Abj18656 Human erb

# ALIGNMENTS

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RESULT 1
AAW23979
ID AAW23979 standard; peptide; 5 AA.
XX
AC AAW23979;
XX
DT 23-JUL-1998 (first entry)
XX
DE Cadherin-mediated cell adhesion modulating peptide 1.
XX
KW Cadherin-mediated; cell adhesion; drug delivery; treatment; cancer;
KW angiogenesis; skin grafting; neurite growth; veterinary medicine;
KW wound healing; tumour; metastasis; carcinoma; leukaemia; modulation;
KW organ transplant; neurological disease.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT Modified-site 5 /note= "optional N-terminal acetylation"
FT Modified-site 5 /note= "optional C-terminal amidation"
XX
XX WO9802452-A2.
XX
XX 22-JAN-1998.
XX
XX 11-JUL-1997; 97WO-CA000489.
XX
XX 12-JUL-1996; 96US-0021612P.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Blaschuk OW, Gour BJ;
XX
XX WPI; 1998-110522/10.
XX
XX Cyclic peptide(s) that modulate cadherin-mediated cell adhesion - used to
XX improve drug delivery through skin, to the brain etc., for treatment of
XX cancer, angiogenesis etc., and to improve grafting of foreign tissue or
XX neurite growth.
XX
XX Claim 8; Page 97; 133pp; English.
XX
XX This is a cyclised peptide capable of modulating cadherin-mediated cell
XX adhesion. Cadherin-expressing cells can be detected from their reaction
XX with the antibody that binds the peptides of the invention. These
XX peptides are useful in human or veterinary medicine to modulate adhesion
XX mediated by E-, N-, P- or R-cadherins (or other cadherins that include
XX the amino acids HAV recognition sequence), specifically where these are
XX expressed by epithelial, endothelial, neural or tumour cells or
XX lymphocytes. The peptides which inhibit cell adhesion are used to improve
XX delivery of drugs through the skin (such that the peptides enters the
XX blood stream), to tumours (particularly ovarian or bladder tumours or
XX melanoma) and to the brain. They are also used to treat cancer
XX (carcinoma, leukaemia or melanoma), inhibit metastasis and also inhibit
XX angiogenesis. The peptides that stimulate adhesion are used to improve
XX wound healing to promote adherence of foreign tissues (skin grafts or
XX organ transplants), and to improve adherence to tissue culture surfaces
XX and bio-reactors. Other uses of the peptides are to induce apoptosis in
XX cadherin-expressing cells, increase or decrease neurite outgrowth, to
XX treat spinal cord injuries and de-myelinating neurological diseases
XX (specifically multiple sclerosis). They can be used for modulating the
XX immune system (e.g. in cases of diabetes or rheumatoid arthritis), for
XX preventing pregnancy and to increase vaso-permeability. The antibodies
XX which bind to these peptides are also used to modulate cell adhesion and

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CC when coupled to a drug, to target the drug to cadherin-expressing cells.
CC Diagnostic agents may also be delivered using the peptides in a skin
CC patch, particularly where the agent generates a colour in contact with,
CC e.g. cocaine, human immunodeficiency viral proteins, glucose or prostate-
CC specific antigen, particularly for home-testing kits. The peptides make
CC it possible to deliver a wide range of drugs through the skin, avoiding
CC parental administration, by-passing the gastro- intestinal system and
CC improving patient compliance
XX
XX Sequence 5 AA;
SQ
Query Match 100.0%; Score 34; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 1 CHAVC 5
|||||
RESULT 2
AAW91033
ID AAW91033 standard; peptide; 5 AA.
XX
AC AAW91033;
XX
DT 24-MAR-1999 (first entry)
XX
DE Peptide inhibiting interaction of alpha-catenin and beta-catenin.
XX
KW Alpha-catenin; beta-catenin; interaction; modulation; cell adhesion;
KW cadherin-mediated function; demyelinating neurological disease;
KW multiple sclerosis; drug delivery; cancer; angiogenesis; immune system;
KW central nervous system; apoptosis induction; cadherin-expression cell;
KW pregnancy prevention; vasopermeability; synaptic stability; diabetes;
KW rheumatoid arthritis; allergic response; learning; memory;
KW antibody-mediated graft rejection; cyclic.
XX
OS Synthetic.
XX
XX WO9845319-A2.
XX
XX 15-OCT-1998.
XX
XX 14-APR-1998; 98WO-CA000322.
XX
XX 10-APR-1997; 97US-0043361P.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Blaschuk OW, Gour BJ;
XX
XX WPI; 1999-024009/02.
XX
XX New catenin modulating agents - comprising peptides having a sequence HAV
XX or analogues or antibodies, used for modulating cadherin-mediated
XX functions.
XX
XX Claim 12; Page 78; 106pp; English.
XX
XX The present sequence represents a peptide which is capable of inhibiting
XX an interaction between alpha-catenin and beta-catenin. The peptide is
XX used in modulating agents that are used for modulating cadherin-mediated
XX functions. They can be used for disrupting interaction between alpha-
XX catenin and beta-catenin in a cell, inhibiting cell adhesion, e.g.
XX between epithelial cells, endothelial cells, neural cells, tumour cells
XX and lymphocytes, for treating a demyelinating neurological disease, e.g.
XX multiple sclerosis, for reducing unwanted cellular adhesion in a mammal,
XX for enhancing the delivery of a drug to a tumour in a mammal, for
XX enhancing the delivery of a drug to a tumour in a mammal, for treating
XX cancer in a mammal, for inhibiting angiogenesis in a mammal, for
XX enhancing drug delivery to the central nervous system of a mammal, for
XX inducing apoptosis in a cadherin-expression cell, for modulating the

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CC immune system of a mammal, for preventing pregnancy in a mammal, for  
 CC increasing vasopermeability in a mammal, or for inhibiting synaptic  
 CC stability in a mammal. In particular they can be used for treating  
 CC diabetes, rheumatoid arthritis, allergic responses, antibody-mediated  
 CC graft rejection or for stimulating learning and memory  
 XX  
 XX Sequence 5 AA;  
 SQ Query Match 100.0%; Score 34; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CHAVC 5  
 Db 1 CHAVC 5

RESULT 3  
 AAW91021  
 ID AAW91021 standard; peptide; 5 AA.  
 XX AC AAW91021;  
 XX DT 24-MAR-1999 (first entry)  
 XX DE Peptide inhibiting interaction of alpha-catenin and beta-catenin.  
 XX KW Alpha-catenin; beta-catenin; interaction; modulation; cell adhesion;  
 KW cadherin-mediated function; demyelinating neurological disease;  
 KW multiple sclerosis; drug delivery; cancer; angiogenesis; immune system;  
 KW central nervous system; apoptosis induction; cadherin-expression cell;  
 KW pregnancy prevention; vasopermeability; synaptic stability; diabetes;  
 KW rheumatoid arthritis; allergic response; learning; memory;  
 KW antibody-mediated graft rejection.  
 XX OS Synthetic.  
 XX W09845319-A2.  
 XX PN 15-OCT-1998.  
 XX PD 14-APR-1998; 98WO-CA000322.  
 XX PF 10-APR-1997; 97US-00433361P.  
 XX PR (UYMC-) UNIV MCGILL.  
 XX PA Blaschuk OW, Gour BJ;  
 XX PI WPI; 1999-024009/02.  
 XX DR New catenin modulating agents - comprising peptides having a sequence HAV  
 XX PT or analogues or antibodies, used for modulating cadherin-mediated  
 XX PT functions.  
 XX PS Claim 10; Page 77; 106pp; English.  
 XX CC The present sequence represents a peptide which is capable of inhibiting  
 CC an interaction between alpha-catenin and beta-catenin. The peptide is  
 CC used in modulating agents that are used for modulating cadherin-mediated  
 CC functions. They can be used for disrupting interaction between alpha-  
 CC catenin and beta-catenin in a cell, inhibiting cell adhesion, e.g.  
 CC between epithelial cells, endothelial cells, neural cells, tumour cells  
 CC and lymphocytes, for treating a demyelinating neurological disease, e.g.  
 CC multiple sclerosis, for reducing unwanted cellular adhesion in a mammal,  
 CC for enhancing the delivery of a drug through the skin of a mammal, for  
 CC enhancing the delivery of a drug to a tumour in a mammal, for treating  
 CC cancer in a mammal, for inhibiting angiogenesis in a mammal, for  
 CC enhancing drug delivery to the central nervous system of a mammal, for  
 CC inducing apoptosis in a cadherin-expression cell, for modulating the  
 CC immune system of a mammal, for preventing pregnancy in a mammal, for  
 CC increasing vasopermeability in a mammal, or for inhibiting synaptic  
 CC stability in a mammal. In particular they can be used for treating

CC diabetes, rheumatoid arthritis, allergic responses, antibody-mediated  
 CC graft rejection or for stimulating learning and memory  
 XX  
 XX Sequence 5 AA;  
 SQ Query Match 100.0%; Score 34; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CHAVC 5  
 Db 1 CHAVC 5

RESULT 4  
 AAY17108  
 ID AAY17108 standard; peptide; 5 AA.  
 XX AC AAY17108;  
 XX DT 20-SEP-1999 (first entry)  
 XX DE Cadherin-mediated adhesion modulating cyclic peptide.  
 XX KW Cell adhesion modulation; CAM; synaptic stability; cadherin;  
 KW cadherin-mediated adhesion; drug delivery; cell adhesion; tumour;  
 KW wound healing; neurite outgrowth; cyclic; circular.  
 XX OS Synthetic.  
 XX W09933875-A1.  
 XX PN 08-JUL-1999.  
 XX PD 23-DEC-1998; 98WO-CA001207.  
 XX PF 23-DEC-1997; 97US-00996679.  
 XX PR (UYMC-) UNIV MCGILL.  
 XX PA Blaschuk OW, Gour BJ;  
 XX PI WPI; 1999-430231/36.  
 XX DR Cyclic peptide cell adhesion modulating agents, useful for modulating  
 XX PT synaptic stability.  
 XX PS Claim 8; Page 64; 144pp; English.  
 XX CC The invention provides cyclic peptide cell adhesion modulating (CAM)  
 CC agents that comprises a His-Ala-Val recognition sequence. Also provided  
 CC is a method for inhibiting synaptic stability in a mammal that comprises  
 CC administering to a mammal a therapeutically effective amount of a CAM  
 CC agent that inhibits cadherin-mediated adhesion, where the agent comprises  
 CC a cyclic peptide having a peptide ring, and where the sequence His-Ala-  
 CC Val is present within the peptide ring. The cyclic peptides are cell  
 CC adhesion modulating agents that inhibit cadherin-mediated adhesion. They  
 CC can be used in a method for inhibiting synaptic stability in mammals. The  
 CC agents can be used to treat diseases or other conditions characterized by  
 CC undesirable cell adhesion or to facilitate drug delivery to a specific  
 CC tissue or tumour. Alternatively the agents may be used to enhance cell  
 CC adhesion (e.g. to supplement or replace stitches or to facilitate wound  
 CC healing) or to enhance or direct neurite outgrowth  
 XX  
 XX Sequence 5 AA;  
 SQ Query Match 100.0%; Score 34; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CHAVC 5  
 Db 1 CHAVC 5

RESULT 5  
 AAB27334 ID AAB27334 standard; peptide; 5 AA.  
 XX AC AAB27334;  
 XX DT 15-FEB-2001 (first entry)  
 XX DE Beta-catenin derived linear peptide SEQ ID NO: 22.  
 XX KW Beta-catenin; cadherin-mediated intercellular adhesion;  
 KW cell differentiation; modulating agent; hair loss; skin exfoliation;  
 KW internalisation moiety; flanking sequence; transcription; hearing loss.  
 XX OS Unidentified.  
 XX WO200053632-A1.  
 XX PN 14-SEP-2000.  
 XX PF 07-MAR-2000; 2000WO-CA000222.  
 XX PR 09-MAR-1999; 99US-00265107.  
 XX PA (UYMC-) UNIV MCGILL.  
 XX PI Blaschuk OW, Gour BJ;  
 XX DR WPI; 2000-594308/56.  
 XX PT Stimulating beta-catenin mediated gene expression, cellular  
 PT differentiation and hair growth, involves contacting cells with  
 PT modulating agent capable of inhibiting interaction between alpha and beta  
 PT catenin.  
 XX PS Disclosure; Page 6; 77pp; English.  
 XX CC The present invention is concerned with methods of modulating the amount  
 CC of free beta-catenin in the cell, and methods of stimulating the  
 CC expression of genes involved in cellular differentiation, the  
 CC transcription of which is under the control of beta-catenin. The peptides  
 CC given in AAB27053-B27088, AAB27284-B27300 and AAB27330-B27351 can be used  
 CC as modulating agents which interrupt the interaction between alpha and  
 CC beta catenin, causing increased levels of the latter and stimulating the  
 CC activation of beta-catenin mediated transcription. This can be used to  
 CC stimulate cell differentiation, which can then be used to promote hair  
 CC growth and skin exfoliation. This latter is particularly useful in the  
 CC improvement of photodamaged skin and to minimise wrinkles. The modulating  
 CC peptide can also be used to reduce hearing loss resulting from inner ear  
 CC disorders such as hyperacusis and tinnitus  
 XX SQ Sequence 5 AA;  
 Query Match 100.0%; Score 34; DB 3; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CHAVC 5  
 Db |||||  
 1 CHAVC 5  
 RESULT 6  
 AAB27346 ID AAB27346 standard; peptide; 5 AA.  
 XX AC AAB27346;  
 XX DT 15-FEB-2001 (first entry)  
 XX DE Beta-catenin derived cyclic peptide SEQ ID NO: 34.

XX KW Beta-catenin; cadherin-mediated intercellular adhesion;  
 KW cell differentiation; modulating agent; hair loss; skin exfoliation;  
 KW internalisation moiety; flanking sequence; transcription; hearing loss;  
 KW cyclic.  
 XX OS Unidentified.  
 XX FH Key Location/Qualifiers  
 FT Disulfide-bond 1..5 /note= "the disulfide bond cyclises the molecule"  
 XX PN WO200053632-A1.  
 XX PD 14-SEP-2000.  
 XX PF 07-MAR-2000; 2000WO-CA000222.  
 XX PR 09-MAR-1999; 99US-00265107.  
 XX PA (UYMC-) UNIV MCGILL.  
 XX PI Blaschuk OW, Gour BJ;  
 XX DR WPI; 2000-594308/56.  
 XX PT Stimulating beta-catenin mediated gene expression, cellular  
 PT differentiation and hair growth, involves contacting cells with  
 PT modulating agent capable of inhibiting interaction between alpha and beta  
 PT catenin.  
 XX PS Disclosure; Page 7; 77pp; English.  
 XX CC The present invention is concerned with methods of modulating the amount  
 CC of free beta-catenin in the cell, and methods of stimulating the  
 CC expression of genes involved in cellular differentiation, the  
 CC transcription of which is under the control of beta-catenin. The peptides  
 CC given in AAB27053-B27088, AAB27284-B27300 and AAB27330-B27351 can be used  
 CC as modulating agents which interrupt the interaction between alpha and  
 CC beta catenin, causing increased levels of the latter and stimulating the  
 CC activation of beta-catenin mediated transcription. This can be used to  
 CC stimulate cell differentiation, which can then be used to promote hair  
 CC growth and skin exfoliation. This latter is particularly useful in the  
 CC improvement of photodamaged skin and to minimise wrinkles. The modulating  
 CC peptide can also be used to reduce hearing loss resulting from inner ear  
 CC disorders such as hyperacusis and tinnitus  
 XX SQ Sequence 5 AA;  
 Query Match 100.0%; Score 34; DB 3; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CHAVC 5  
 Db |||||  
 1 CHAVC 5  
 RESULT 7  
 AAY73790 ID AAY73790 standard; peptide; 5 AA.  
 XX AC AAY73790;  
 XX DT 07-MAR-2000 (first entry)  
 XX DE N-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:296.  
 XX KW Diagnosis; cancer; OB-cadherin; N-cadherin; E-cadherin; CAR; cyclic;  
 KW cell adhesion recognition sequence; leukaemia; metastasis;  
 KW prostate cancer; breast cancer; ovarian cancer; carcinoma.  
 XX OS Synthetic.





```

FT Modified-site 5 /note= "Linked to residue 1 to form a cyclic peptide, C-
PT terminal amide"
XX
XX
XX WO200177146-A2.
XX
XX 18-OCT-2001.
XX
XX 09-APR-2001; 2001WO-US011669.
XX
XX 07-APR-2000; 2000US-00544782.
XX (UYMC-) UNIV MCGILL.
XX
XX Blaschuk OW, Gour BJ, Farookhi R, Ali A;
XX WPI; 2002-049129/06.
XX
XX Modulating endothelial cell adhesion for inhibiting development of
PT endometriosis, increasing blood flow to tumor in a mammal, by contacting
PT cell with a cyclic peptide having cadherin cell adhesion recognition
PT sequence.
XX
XX Claim 6; Page 64; 139pp; English.
XX
XX The present invention relates to a method for modulating endothelial cell
CC adhesion. The method comprises contacting an endothelial cell with a
CC modulating peptide comprising a cadherin cell adhesion recognition
CC sequence (His Ala Val) within a cyclic peptide ring. The method is useful
CC for inhibiting angiogenesis, increasing vasopermeability, increasing
CC blood flow to a tumour, disrupting neovasculation and inhibiting the
CC development of endometriosis in a mammal. The modulating peptide reduces
CC unwanted endothelial adhesion occurring between tumour cells, tumour
CC cells and normal cells, normal cells as a result of surgery, injury,
CC chemotherapy, disease and inflammation. The present sequence is one such
CC modulating peptide
XX
XX Sequence 5 AA;
XX
XX Query Match 100.0%; Score 34; DB 5; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CHAVC 5
XX |||||
XX Db 1 CHAVC 5
XX
XX RESULT 10
XX ABU60211
XX ID ABU60211 standard; peptide; 5 AA.
XX
XX AC ABU60211;
XX
XX 24-APR-2003 (first entry)
XX
XX DE N-cadherin cell adhesion recognition sequence #1.
XX
XX KW Metastasis; cancer; binding agent; cell adhesion recognition; CAR;
XX OB-cadherin; N-cadherin; prostate cancer; ovarian cancer; breast cancer;
XX leukaemia.
XX
XX KW
XX OS Synthetic.
XX
XX US2002146687-A1.
XX
XX 10-OCT-2002.
XX
XX 05-MAY-1999; 99US-00305928.
XX
XX 05-MAY-1998; 98US-00073040.
XX
XX 06-NOV-1998; 98US-00187859.
XX
XX 20-JAN-1999; 99US-00234395.
XX

XX (BLAS/) BLASCHUK O W.
XX (SYMO/) SYMONDS J M.
XX (BYER/) BYERS S.
XX (GOUR/) GOUR B J.
XX
XX Blaschuk OW, Symonds JM, Byers S, Gour BJ;
XX WPI; 2003-255125/25.
XX
XX Diagnosing or evaluating metastatic potential of cancer in patient by
PT contacting biological sample obtained from patient with specified binding
PT agent or oligonucleotide, and detecting polypeptide that binds to the
PT binding agent.
XX
XX Disclosure; Page 8; 94pp; English.
XX
XX The invention discloses a method for diagnosing or evaluating metastatic
CC potential of cancer in a patient. The method comprises contacting a
CC biological sample obtained from the patient with a binding agent,
CC preferentially antibodies or cell adhesion recognition (CAR) sequences,
CC that specifically bind to OB-cadherin or N-cadherin or an oligonucleotide
CC that hybridises to a polynucleotide encoding OB-cadherin or N-cadherin
CC and then detecting the amount of polypeptide that binds to the binding
CC agent. The inventive method is useful for diagnosing or evaluating
CC metastatic potential of cancer, such as prostate, ovarian or breast
CC cancer, as well as leukaemia in a patient. It can also be employed for
CC monitoring the progression of cancer in a patient. The inventive method
CC provides accurate diagnosis or evaluation of metastatic potential of
CC cancer in a patient in a simple and economical manner. The sequences
CC presented in ABUS9926-ABUS9969 and ABU60211-ABU60229 are OB-cadherin or N
CC -cadherin, respectively, CAR sequences
XX
XX Sequence 5 AA;
XX
XX Query Match 100.0%; Score 34; DB 6; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CHAVC 5
XX |||||
XX Db 1 CHAVC 5
XX
XX RESULT 11
XX ABO43539
XX ID ABO43539 standard; peptide; 5 AA.
XX
XX AC ABO43539;
XX
XX DT 25-SEP-2003 (first entry)
XX
XX DE Classical cadherin CAR sequence cyclic peptide peptidomimetic #1.
XX
XX KW Cadherin; CAD; extracellular domain; cell adhesion; peptidomimetic;
XX cadherin-mediated intercellular adhesion; tumour; cancer; angiogenesis;
XX central nervous system; wound healing; vasopermeability; N-cadherin;
XX demyelinating neurological disease; astrocyte; synaptic stability; ovary;
XX neurite outgrowth; spinal cord injury; macular degeneration; bladder;
XX melanoma; carcinoma; leukaemia; skin disorder; acute B cell leukaemia;
XX immune reaction; immunoglobulin; T cell generation; CAR; cyclic;
XX cell adhesion recognition sequence.
XX
XX OS Synthetic.
XX
XX US2002168761-A1.
XX
XX 14-NOV-2002.
XX
XX 24-JAN-2001; 2001US-00769145.
XX
XX 24-JAN-2000; 2000US-00491078.
XX
```

PA (GOUR/) GOUR B J.  
 PA (BLAS/) BLASCHUK O W.  
 PA (ALIA/) ALI A.  
 PA (NIFF/) NI F.  
 PA (CHEN/) CHEN Z.  
 PA (MICH/) MICHAUD S D.  
 PA (WANG/) WANG S.  
 PA (HUZZ/) HU Z.  
 XX GOUR BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;  
 PI Hu Z;  
 XX WPI; 2003-521524/49.  
 XX  
 XX Novel cell adhesion modulating agent for modulating cadherin-mediated  
 PT intercellular adhesion, for enhancing wound healing, has three-  
 PT dimensional structure similar to three-dimensional structure of cyclic  
 PT peptide.  
 XX  
 XX Claim 15; Page 99; 309pp; English.  
 XX  
 XX The invention relates to a cell adhesion modulating agent which is a  
 CC peptidomimetic having a three-dimensional structure of a cyclic peptide  
 CC that comprises the sequence HAV within a cyclic peptide ring. The agent  
 CC is useful for modulating classical cadherin-mediated intercellular  
 CC adhesion, for reducing unwanted cellular adhesion in a mammal, for  
 CC enhancing the delivery of a drug to a tumour, for inhibiting the  
 CC development of cancer, for inhibiting angiogenesis, for enhancing drug  
 CC delivery to the central nervous system, for enhancing wound healing, for  
 CC enhancing the adhesion of foreign tissue implanted within a mammal, for  
 CC modulating the immune system of a mammal, for increasing  
 CC vasopermeability, for treating a demyelinating neurological disease, for  
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,  
 CC for inhibiting synaptic stability, for modulating neurite outgrowth, for  
 CC treating spinal cord injuries and for treating macular degeneration. The  
 CC cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or  
 CC leukaemia. The agent is useful for treating skin disorders, acute B cell  
 CC leukaemia, excessive immune reactions involving the humoral immune system  
 CC and generation of immunoglobulins and diseases associated with excessive  
 CC generation of T cells. This sequence represents a cadherin (CAD) cell  
 CC adhesion recognition (CAR) sequence cyclic peptide peptidomimetic of the  
 CC invention  
 XX  
 XX Sequence 5 AA;  
 SQ  
 Query Match 100.0%; Score 34; DB 7; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CHAVC 5  
 DB 1 CHAVC 5  
 RESULT 12  
 ADK13544  
 ID ADK13544 standard; peptide; 5 AA.  
 XX  
 AC ADK13544;  
 XX  
 XX 17-JUN-2004 (first entry)  
 DT  
 XX  
 XX Cadherin-mediated cell adhesion-modulating peptidomimetic #3.  
 DE  
 XX Cell adhesion-modulating agent; cadherin-mediated cell adhesion; cancer;  
 KW angiogenesis; central nervous system; wound healing;  
 KW foreign tissue adhesion; vasopermeability;  
 KW demyelinating neurological disease; astrocyte; synaptic stability;  
 KW neurite outgrowth; spinal cord injury; macular degeneration; metastasis;  
 KW bladder; tumour; ovary; melanoma; carcinoma; leukaemia;  
 KW multiple sclerosis; cytostatic; antiangiogenic; neuroprotective;  
 KW ophthalmological; Cell adhesion-modulating peptidomimetic;  
 KW cadherin cell adhesion recognition sequence; CAR; cyclic.

XX Synthetic.  
 OS US2004058864-A1.  
 PN 25-MAR-2004.  
 XX  
 PD 10-APR-2003; 2003US-00412701.  
 XX  
 XX 24-JAN-2000; 2000US-00491078.  
 PR 24-JAN-2001; 2001US-00769145.  
 XX  
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
 PA  
 XX GOUR BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;  
 PI Hu Z;  
 XX WPI; 2004-268836/25.  
 DR  
 XX  
 XX New cell adhesion modulating agent, useful for treating or preventing  
 PT cancer and/or inhibiting metastasis, inhibiting angiogenesis, enhancing  
 PT wound healing, treating a demyelinating neurological disease or treating  
 PT spinal cord injuries.  
 XX  
 XX Claim 15; SEQ ID NO 10; 281pp; English.  
 PS  
 XX The invention relates to a cell adhesion-modulating agent. The invention  
 CC also relates to methods for screening a candidate compound for the  
 CC ability to modulate classical cadherin-mediated cell adhesion,  
 CC identifying a compound that modulates classical cadherin-mediated cell  
 CC adhesion, modulating classical cadherin-mediated intercellular adhesion,  
 CC reducing unwanted cellular adhesion in a mammal, enhancing the delivery  
 CC of a drug to a tumour in a mammal, inhibiting the development of a cancer  
 CC in a mammal, inhibiting angiogenesis in a mammal, enhancing drug delivery  
 CC to the central nervous system of a mammal, enhancing wound healing in a  
 CC mammal, enhancing adhesion of foreign tissue implanted within a mammal,  
 CC modulating the immune system of a mammal, increasing vasopermeability in  
 CC a mammal, treating a demyelinating neurological disease in a mammal,  
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,  
 CC inhibiting synaptic stability in a mammal, modulating neurite outgrowth,  
 CC treating spinal cord injuries in a mammal and treating macular  
 CC degeneration in a mammal. The compounds are useful for inhibiting or  
 CC enhancing cadherin-mediated cell adhesion. The cell adhesion modulating  
 CC agents are useful for inhibiting the development of cancer, e.g. treating  
 CC or preventing cancer and/or inhibiting metastasis. The cancer is a  
 CC bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The  
 CC agents are also useful in inhibiting angiogenesis, for enhancing the  
 CC delivery of a drug to a tumour in a mammal, for enhancing wound healing in  
 CC to the central nervous system of a mammal, for enhancing drug delivery  
 CC a mammal, for enhancing adhesion of foreign tissue implanted within a  
 CC mammal, for modulating the immune system of a mammal, for treating a  
 CC demyelinating neurological disease (such as multiple sclerosis) in a  
 CC mammal, for inhibiting synaptic stability in a mammal, for modulating  
 CC neurite outgrowth, for treating spinal cord injuries in a mammal and for  
 CC treating macular degeneration in a mammal. This sequence represents a  
 CC cadherin-mediated cell adhesion-modulating peptidomimetic, comprising a  
 CC classical cadherin cell adhesion recognition (CAR) sequence.  
 XX  
 XX Sequence 5 AA;  
 SQ  
 Query Match 100.0%; Score 34; DB 8; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CHAVC 5  
 DB 1 CHAVC 5  
 RESULT 13  
 AAG65445  
 ID AAG65445 standard; peptide; 6 AA.  
 XX

AC	AAG65445;	DE	Cyclic peptide with classical cadherin CAR sequence.
XX		XX	
DT	30-NOV-2001 (first entry)	KW	Cell adhesion; imidazole; peptidomimetic; cadherin; angiogenesis; CAR;
XX		KW	cytostatic; vulnerary; immunomodulator; vasotropic; neuroprotective;
DE	Cyclic peptide with classical cadherin CAR sequence.	KW	cerebroprotective; muscular; cyclic.
XX		XX	
KW	Cell adhesion; imidazole; peptidomimetic; cadherin; angiogenesis; CAR;	OS	Synthetic.
KW	cytostatic; vulnerary; immunomodulator; vasotropic; neuroprotective;	XX	
KW	cerebroprotective; muscular; cyclic.	PH	Key Location/Qualifiers
XX		FT	Modified-site 1
XX		FT	/note= "putative N-terminal acetylation or
FT		FT	alkoxybenzylolation"
FT		FT	Modified-site 6
FT		FT	/note= "putative C-terminal amide or ester"
FT		PN	WO200153331-A2.
XX		XX	
XX		PD	26-JUL-2001.
XX		XX	
PN	WO200153331-A2.	XX	
XX		PF	24-JAN-2001; 2001WO-US002508.
XX		XX	
PD	26-JUL-2001.	XX	
XX		PR	24-JAN-2000; 2000US-00491078.
XX		XX	
XX		PA	(ADHE-) ADHEREX TECHNOLOGIES INC.
XX		XX	
PI	Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;	XX	
PI	Hu Z;	PI	
XX		PI	
XX		XX	
DR	WPI; 2001-549899/61.	DR	
XX		XX	
FT	Cell adhesion modulating agent used for enhancing delivery of drug to	XX	
FT	tumor comprises imidazole compounds.	XX	
XX		PS	Example; Page 412; 436pp; English.
PS		XX	
XX		CC	The invention relates to cell adhesion modulating agents that comprise
CC		CC	imidazole compounds of specified formulae that are peptidomimetics of
CC		CC	cyclic peptides. The peptidomimetics have a structure similar to that of
CC		CC	a cyclic peptide that comprises a cadherin cell recognition sequence HAV.
CC		CC	The agents are used for modulating classical cadherin mediated
CC		CC	intercellular adhesion, reducing unwanted cellular adhesion, enhancing
CC		CC	delivery of a drug to a tumor, inhibiting development of cancer,
CC		CC	inhibiting angiogenesis, enhancing drug delivery to the CNS, enhancing
CC		CC	wound healing, modulating the immune system, increasing vasopermeability,
CC		CC	treating demyelinating disease, facilitating migration of an N-cadherin
CC		CC	expressing cell on astrocytes, inhibiting synaptic stability, modulating
CC		CC	neurite outgrowth, and treating spinal cord injuries and macular
CC		CC	degeneration. The present sequence represents a cyclic peptide with
CC		CC	classical cadherin cell adhesion recognition (CAR) sequence
XX		XX	
SQ	Sequence 6 AA;	XX	
		Query Match	100.0%; Score 34; DB 4; Length 6;
		Best Local Similarity	100.0%; Pred. No. 1.8e+06;
		Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
		QY	1 CHAVC 5
		DB	2 CHAVC 6
		RESULT 14	
		AAG65449	
		ID	AAG65449 standard; peptide; 6 AA.
		XX	
		AC	AAG65449;
		XX	
		DT	30-NOV-2001 (first entry)
		XX	
		KW	Cyclic peptide with classical cadherin CAR sequence.
		XX	
		KW	Cell adhesion; imidazole; peptidomimetic; cadherin; angiogenesis; CAR;
		KW	cytostatic; vulnerary; immunomodulator; vasotropic; neuroprotective;





```
PR 07-APR-2000; 2000US-00544782.
XX (UYMC-) UNIV MCGILL.
PA Blaschuk OW, Gour BJ, Farookhi R, Ali A;
XX WPI; 2002-049129/06.
XX
XX Modulating endothelial cell adhesion for inhibiting development of
XX endometriosis, increasing blood flow to tumor in a mammal, by contacting
XX cell with a cyclic peptide having cadherin cell adhesion recognition
XX sequence.
XX
XX Example 1; Page 49; 139pp; English.
XX
XX The present invention relates to a method for modulating endothelial cell
XX adhesion. The method comprises contacting an endothelial cell with a
XX modulating peptide comprising a cadherin cell adhesion recognition
XX sequence (His Ala Val) within a cyclic peptide ring. The method is useful
XX for inhibiting angiogenesis, increasing vasopermeability, increasing the
XX blood flow to a tumour, disrupting neovasculture and inhibiting the
XX development of endometriosis in a mammal. The modulating peptide reduces
XX unwanted endothelial adhesion occurring between tumour cells, tumour
XX cells and normal cells, normal cells as a result of surgery, injury,
XX chemotherapy, disease and inflammation. The present sequence was used to
XX illustrate the present invention
XX
XX Sequence 6 AA;
SQ
Query Match 100.0%; Score 34; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CHAVC 5
Db 1 CHAVC 5
RESULT '20
AAM47521
XX ID AAM47521 standard; peptide; 6 AA.
XX AC AAM47521;
XX
XX 12-FEB-2002 (first entry)
XX
XX Cyclic peptide endothelial cell adhesion modulator #14.
XX
XX Cadherin; cytostatic; gynecological; endometriosis;
XX endothelial cell adhesion; angiogenesis; vasopermeability; tumour;
XX cyclic.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1 /note= "Linked to residue 6 to form a cyclic peptide, N-
XX terminal acetyl or N-terminal CH3-SO2 group"
XX Modified-site 6 /note= "Linked to residue 1 to form a cyclic peptide, C-
XX terminal amide"
XX
XX WO200177146-A2.
XX
XX 18-OCT-2001.
XX
XX 09-APR-2001; 2001WO-US011669.
XX
XX 07-APR-2000; 2000US-00544782.
XX (UYMC-) UNIV MCGILL.
XX Blaschuk OW, Gour BJ, Farookhi R, Ali A;
XX
XX Modulating endothelial cell adhesion for inhibiting development of
XX endometriosis, increasing blood flow to tumor in a mammal, by contacting
XX cell with a cyclic peptide having cadherin cell adhesion recognition
XX sequence.
XX
XX WPI; 2002-049129/06.
XX
XX Modulating endothelial cell adhesion for inhibiting development of
XX endometriosis, increasing blood flow to tumor in a mammal, by contacting
XX cell with a cyclic peptide having cadherin cell adhesion recognition
XX sequence.
XX
XX Claim 6; Page 64; 139pp; English.
XX
XX The present invention relates to a method for modulating endothelial cell
XX adhesion. The method comprises contacting an endothelial cell with a
XX modulating peptide comprising a cadherin cell adhesion recognition
XX sequence (His Ala Val) within a cyclic peptide ring. The method is useful
XX for inhibiting angiogenesis, increasing vasopermeability, increasing the
XX blood flow to a tumour, disrupting neovasculture and inhibiting the
XX development of endometriosis in a mammal. The modulating peptide reduces
XX unwanted endothelial adhesion occurring between tumour cells, tumour
XX cells and normal cells, normal cells as a result of surgery, injury,
XX chemotherapy, disease and inflammation. The present sequence is one such
XX modulating peptide
XX
XX Sequence 6 AA;
SQ
Query Match 100.0%; Score 34; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CHAVC 5
Db 2 CHAVC 6
RESULT 21
AAM47555
XX ID AAM47555 standard; peptide; 6 AA.
XX AC AAM47555;
XX
XX 12-FEB-2002 (first entry)
XX
XX Cyclic peptide endothelial cell adhesion modulator #37.
XX
XX Cadherin; cytostatic; gynecological; endometriosis;
XX endothelial cell adhesion; angiogenesis; vasopermeability; tumour;
XX cyclic.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1 /note= "Linked to residue 6 to form a cyclic peptide, N-
XX terminal acetyl"
XX Modified-site 6 /note= "Linked to residue 1 to form a cyclic peptide, C-
XX terminal amide"
XX
XX WO200177146-A2.
XX
XX 18-OCT-2001.
XX
XX 09-APR-2001; 2001WO-US011669.
XX
XX 07-APR-2000; 2000US-00544782.
XX (UYMC-) UNIV MCGILL.
XX Blaschuk OW, Gour BJ, Farookhi R, Ali A;
XX
XX WPI; 2002-049129/06.
XX
XX Modulating endothelial cell adhesion for inhibiting development of
XX endometriosis, increasing blood flow to tumor in a mammal, by contacting
```

PT cell with a cyclic peptide having cadherin cell adhesion recognition  
PT sequence.  
XX  
PS Disclosure; Page 5; 139pp; English.  
XX  
CC The present invention relates to a method for modulating endothelial cell  
CC adhesion. The method comprises contacting an endothelial cell with a  
CC modulating peptide comprising a cadherin cell adhesion recognition  
CC sequence (His Ala Val) within a cyclic peptide ring. The method is useful  
CC for inhibiting angiogenesis, increasing vasopermeability, increasing  
CC blood flow to a tumour, disrupting neovasculature and inhibiting the  
CC development of endometriosis in a mammal. The modulating peptide reduces  
CC unwanted endothelial adhesion occurring between tumour cells, tumour  
CC cells and normal cells, normal cells as a result of surgery, injury,  
CC chemotherapy, disease and inflammation. The present sequence is one such  
CC modulating peptide  
XX  
SQ Sequence 6 AA;  
Query Match 100.0%; Score 34; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CHAVC 5  
Db 2 CHAVC 6  
RESULT 22  
AAM47554  
ID AAM47554 standard; peptide; 6 AA.  
XX  
AC AAM47554;  
XX  
DT 12-FEB-2002 (first entry)  
XX  
DE Cyclic peptide endothelial cell adhesion modulator #16.  
XX  
DE Cadherin; cytostatic; gynecological; endometriosis;  
KW endothelial cell adhesion; angiogenesis; vasopermeability; tumour;  
KW cyclic.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /note= "Linked to residue 6 to form a cyclic peptide, N-  
FT terminal acetyl or N-terminal CH3-SO2 group"  
FT Modified-site 6  
FT /note= "Linked to residue 1 to form a cyclic peptide, C-  
FT terminal amide"  
XX  
PN WO200177146-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 09-APR-2001; 2001WO-US011669.  
XX  
PR 07-APR-2000; 2000US-00544782.  
XX  
PA (UYMC-) UNIV MCGILL.  
XX  
PI Blaschuk OW, Gour BJ, Farookhi R, Ali A;  
XX  
DR WPI; 2002-049129/06.  
XX  
PT Modulating endothelial cell adhesion for inhibiting development of  
PT endometriosis, increasing blood flow to tumor in a mammal, by contacting  
PT cell with a cyclic peptide having cadherin cell adhesion recognition  
PT sequence.  
XX  
PS Claim 6; Page 64; 139pp; English.

CC The present invention relates to a method for modulating endothelial cell  
CC adhesion. The method comprises contacting an endothelial cell with a  
CC modulating peptide comprising a cadherin cell adhesion recognition  
CC sequence (His Ala Val) within a cyclic peptide ring. The method is useful  
CC for inhibiting angiogenesis, increasing vasopermeability, increasing  
CC blood flow to a tumour, disrupting neovasculature and inhibiting the  
CC development of endometriosis in a mammal. The modulating peptide reduces  
CC unwanted endothelial adhesion occurring between tumour cells, tumour  
CC cells and normal cells, normal cells as a result of surgery, injury, such  
CC chemotherapy, disease and inflammation. The present sequence is one  
CC modulating peptide  
XX  
SQ Sequence 6 AA;  
Query Match 100.0%; Score 34; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CHAVC 5  
Db 1 CHAVC 5  
RESULT 23  
AAM47558  
ID AAM47558 standard; peptide; 6 AA.  
XX  
AC AAM47558;  
XX  
DT 12-FEB-2002 (first entry)  
XX  
DE Cyclic peptide endothelial cell adhesion modulator #19.  
XX  
DE Cadherin; cytostatic; gynecological; endometriosis;  
KW endothelial cell adhesion; angiogenesis; vasopermeability; tumour;  
KW cyclic.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /note= "Linked to residue 6 to form a cyclic peptide, N-  
FT terminal acetyl or N-terminal CH3-SO2 group"  
FT Modified-site 6  
FT /note= "Linked to residue 1 to form a cyclic peptide, C-  
FT terminal amide"  
XX  
PN WO200177146-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 09-APR-2001; 2001WO-US011669.  
XX  
PR 07-APR-2000; 2000US-00544782.  
XX  
PA (UYMC-) UNIV MCGILL.  
XX  
PI Blaschuk OW, Gour BJ, Farookhi R, Ali A;  
XX  
DR WPI; 2002-049129/06.  
XX  
PT Modulating endothelial cell adhesion for inhibiting development of  
PT endometriosis, increasing blood flow to tumor in a mammal, by contacting  
PT cell with a cyclic peptide having cadherin cell adhesion recognition  
PT sequence.  
XX  
PS Claim 6; Page 64; 139pp; English.  
XX  
CC The present invention relates to a method for modulating endothelial cell  
CC adhesion. The method comprises contacting an endothelial cell with a  
CC modulating peptide comprising a cadherin cell adhesion recognition  
CC sequence (His Ala Val) within a cyclic peptide ring. The method is useful  
CC for inhibiting angiogenesis, increasing vasopermeability, increasing



CC blood flow to a tumour, disrupting neovasculature and inhibiting the  
CC development of endometriosis in a mammal. The modulating peptide reduces  
CC unwanted endothelial adhesion occurring between tumour cells, tumour  
CC cells and normal cells, normal cells as a result of surgery, injury,  
CC chemotherapy, disease and inflammation. The present sequence is one such  
CC modulating peptide  
XX  
SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. NO. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
DB 1 CHAVC 5

RESULT 24  
AAM47560  
ID AAM47560 standard; peptide; 6 AA.

AC AAM47560;

XX 12-FEB-2002 (first entry)

DE Cyclic peptide endothelial cell adhesion modulator #21.

XX Cadherin; cytostatic; gynecological; endometriosis;  
KW endothelial cell adhesion; angiogenesis; vasopermeability; tumour;  
KW cyclic.  
KW  
OS Synthetic.

Key Location/Qualifiers  
FH Key 1

FT Modified-site 1 /note= "Linked to residue 6 to form a cyclic peptide, N-  
terminal acetyl or N-terminal CH3-SO2 group"

FT Modified-site 6 /note= "Linked to residue 1 to form a cyclic peptide, C-  
terminal amide"

FT WO200177146-A2.

PN 18-OCT-2001.

XX 09-APR-2001; 2001WO-US011669.

XX 07-APR-2000; 2000US-00544782.

XX (UYMC-) UNIV MCGILL.

XX Blaschuk OW, Gour BJ, Farookhi R, Ali A;

XX WPI; 2002-049129/06.

XX Modulating endothelial cell adhesion for inhibiting development of  
PT endometriosis, increasing blood flow to tumor in a mammal, by contacting  
PT cell with a cyclic peptide having cadherin cell adhesion recognition  
PT sequence.

XX Claim 6; Page 64; 139pp; English.

XX The present invention relates to a method for modulating endothelial cell  
CC adhesion. The method comprises contacting an endothelial cell with a  
CC modulating peptide comprising a cadherin cell adhesion recognition  
CC sequence (His Ala Val) within a cyclic peptide ring. The method is useful  
CC for inhibiting angiogenesis, increasing vasopermeability, increasing  
CC blood flow to a tumour, disrupting neovasculature and inhibiting the  
CC development of endometriosis in a mammal. The modulating peptide reduces  
CC unwanted endothelial adhesion occurring between tumour cells, tumour  
CC cells and normal cells, normal cells as a result of surgery, injury,  
CC chemotherapy, disease and inflammation. The present sequence is one such

CC modulating peptide  
XX  
SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. NO. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
DB 1 CHAVC 5

RESULT 25  
AAM47559  
ID AAM47559 standard; peptide; 6 AA.

XX AAM47559;

XX 12-FEB-2002 (first entry)

DE Cyclic peptide endothelial cell adhesion modulator #20.

XX Cadherin; cytostatic; gynecological; endometriosis;  
KW endothelial cell adhesion; angiogenesis; vasopermeability; tumour;  
KW cyclic.  
KW  
OS Synthetic.

Key Location/Qualifiers  
FH Key 1

FT Modified-site 1 /note= "Linked to residue 6 to form a cyclic peptide, N-  
terminal acetyl or N-terminal CH3-SO2 group"

FT Modified-site 6 /note= "Linked to residue 1 to form a cyclic peptide, C-  
terminal amide"

FT WO200177146-A2.

PN 18-OCT-2001.

XX 09-APR-2001; 2001WO-US011669.

XX 07-APR-2000; 2000US-00544782.

XX (UYMC-) UNIV MCGILL.

XX Blaschuk OW, Gour BJ, Farookhi R, Ali A;

XX WPI; 2002-049129/06.

XX Modulating endothelial cell adhesion for inhibiting development of  
PT endometriosis, increasing blood flow to tumor in a mammal, by contacting  
PT cell with a cyclic peptide having cadherin cell adhesion recognition  
PT sequence.

XX Claim 6; Page 64; 139pp; English.

XX The present invention relates to a method for modulating endothelial cell  
CC adhesion. The method comprises contacting an endothelial cell with a  
CC modulating peptide comprising a cadherin cell adhesion recognition  
CC sequence (His Ala Val) within a cyclic peptide ring. The method is useful  
CC for inhibiting angiogenesis, increasing vasopermeability, increasing  
CC blood flow to a tumour, disrupting neovasculature and inhibiting the  
CC development of endometriosis in a mammal. The modulating peptide reduces  
CC unwanted endothelial adhesion occurring between tumour cells, tumour  
CC cells and normal cells, normal cells as a result of surgery, injury,  
CC chemotherapy, disease and inflammation. The present sequence is one such  
CC modulating peptide

XX Sequence 6 AA;

Query Match 100.0%; Score 34; DB 5; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.8e+06; Mismatches 0; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
      |||||  
Db 1 CHAVC 5

RESULT 26  
ABO43613  
ID ABO43613 standard; peptide; 6 AA.  
XX  
AC ABO43613;  
XX  
DT 25-SEP-2003 (first entry)  
XX  
DE Classical cadherin CAR sequence cyclic peptide peptidomimetic #73.  
XX  
KW Cadherin; CAD; extracellular domain; cell adhesion; peptidomimetic;  
KW cadherin-mediated intercellular adhesion; tumour; cancer; angiogenesis;  
KW central nervous system; wound healing; vasopermeability; N-cadherin;  
KW demyelinating neurological disease; astrocyte; synaptic stability; ovary;  
KW neurite outgrowth; spinal cord injury; macular degeneration; bladder;  
KW melanoma; carcinoma; leukaemia; skin disorder; acute B cell leukaemia;  
KW immune reaction; immunoglobulin; T cell generation; CAR; cyclic;  
KW cell adhesion recognition sequence.  
XX  
OS Synthetic.  
XX  
PN US2002168761-A1.  
XX  
PD 14-NOV-2002.  
XX  
PF 24-JAN-2001; 2001US-00769145.  
XX  
PR 24-JAN-2000; 2000US-00491078.  
XX  
PA (GOUR/) GOUR B J.  
PA (BLAS/) BLASCHUK O W.  
PA (ALIA/) ALI A.  
PA (NIFE/) NI F.  
PA (CHEN/) CHEN Z.  
PA (MICH/) MICHAUD S D.  
PA (WANG/) WANG S.  
PA (HUZZ/) HU Z.  
XX  
PI Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;  
PI Hu Z;  
XX  
DR WPI; 2003-521524/49.  
XX  
PT Novel cell adhesion modulating agent for modulating cadherin-mediated  
PT intercellular adhesion, for enhancing wound healing, has three-  
PT dimensional structure similar to three-dimensional structure of cyclic  
PT peptide.  
XX  
PS Disclosure; Page 7; 309pp; English.  
XX  
CC The invention relates to a cell adhesion modulating agent which is a  
CC peptidomimetic having a three-dimensional structure of a cyclic peptide  
CC that comprises the sequence HAV within a cyclic peptide ring. The agent  
CC is useful for modulating classical cadherin-mediated intercellular  
CC adhesion, for reducing unwanted cellular adhesion in a mammal, for  
CC enhancing the delivery of a drug to a tumour, for inhibiting the  
CC development of cancer, for inhibiting angiogenesis, for enhancing drug  
CC delivery to the central nervous system, for enhancing wound healing, for  
CC enhancing the adhesion of foreign tissue implanted within a mammal, for  
CC modulating the immune system of a mammal, for increasing  
CC vasopermeability, for treating a demyelinating neurological disease, for  
CC facilitating migration of an N-cadherin expressing cell on astrocytes,  
CC for inhibiting synaptic stability, for modulating neurite outgrowth, for  
CC treating spinal cord injuries and for treating macular degeneration. The  
CC cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or

CC leukaemia. The agent is useful for treating skin disorders, acute B cell  
CC leukaemia, excessive immune reactions involving the humoral immune system  
CC and generation of immunoglobulins and diseases associated with excessive  
CC generation of T cells. This sequence represents a cadherin (CAD) cell  
CC adhesion recognition (CAR) sequence cyclic peptide peptidomimetic of the  
CC invention  
XX  
SQ Sequence 6 AA;  
Query Match 100.0%; Score 34; DB 7; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CHAVC 5  
      |||||  
Db 1 CHAVC 5

RESULT 27  
ABO43610  
ID ABO43610 standard; peptide; 6 AA.  
XX  
AC ABO43610;  
XX  
DT 25-SEP-2003 (first entry)  
XX  
DE Classical cadherin CAR sequence cyclic peptide peptidomimetic #70.  
XX  
KW Cadherin; CAD; extracellular domain; cell adhesion; peptidomimetic;  
KW cadherin-mediated intercellular adhesion; tumour; cancer; angiogenesis;  
KW central nervous system; wound healing; vasopermeability; N-cadherin;  
KW demyelinating neurological disease; astrocyte; synaptic stability; ovary;  
KW neurite outgrowth; spinal cord injury; macular degeneration; bladder;  
KW melanoma; carcinoma; leukaemia; skin disorder; acute B cell leukaemia;  
KW immune reaction; immunoglobulin; T cell generation; CAR; cyclic;  
KW cell adhesion recognition sequence.  
XX  
OS Synthetic.  
XX  
PN US2002168761-A1.  
XX  
PD 14-NOV-2002.  
XX  
PF 24-JAN-2001; 2001US-00769145.  
XX  
PR 24-JAN-2000; 2000US-00491078.  
XX  
PA (GOUR/) GOUR B J.  
PA (BLAS/) BLASCHUK O W.  
PA (ALIA/) ALI A.  
PA (NIFE/) NI F.  
PA (CHEN/) CHEN Z.  
PA (MICH/) MICHAUD S D.  
PA (WANG/) WANG S.  
PA (HUZZ/) HU Z.  
XX  
PI Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;  
PI Hu Z;  
XX  
DR WPI; 2003-521524/49.  
XX  
PT Novel cell adhesion modulating agent for modulating cadherin-mediated  
PT intercellular adhesion, for enhancing wound healing, has three-  
PT dimensional structure similar to three-dimensional structure of cyclic  
PT peptide.  
XX  
PS Claim 15; Page 99; 309pp; English.  
XX  
CC The invention relates to a cell adhesion modulating agent which is a  
CC peptidomimetic having a three-dimensional structure of a cyclic peptide  
CC that comprises the sequence HAV within a cyclic peptide ring. The agent  
CC is useful for modulating classical cadherin-mediated intercellular  
CC adhesion, for reducing unwanted cellular adhesion in a mammal, for

CC enhancing the delivery of a drug to a tumour, for inhibiting the  
 CC development of cancer, for inhibiting angiogenesis, for enhancing drug  
 CC delivery to the central nervous system, for enhancing wound healing, for  
 CC enhancing the adhesion of foreign tissue implanted within a mammal, for  
 CC modulating the immune system of a mammal, for increasing  
 CC vasopermeability, for treating a demyelinating neurological disease, for  
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,  
 CC for inhibiting synaptic stability, for modulating neurite outgrowth, for  
 CC treating spinal cord injuries and for treating macular degeneration. The  
 CC cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or  
 CC leukaemia. The agent is useful for treating skin disorders, acute B cell  
 CC leukaemia, excessive immune reactions involving the humoral immune system  
 CC and generation of immunoglobulins and diseases associated with excessive  
 CC generation of T cells. This sequence represents a cadherin (CAD) cell  
 CC adhesion recognition (CAR) sequence cyclic peptide peptidomimetic of the  
 CC invention  
 XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 34; DB 7; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CHAVC 5  
 Db |||||  
 1 CHAVC 5  
 RESULT 28  
 ABO43617  
 ID ABO43617 standard; peptide; 6 AA.  
 XX  
 AC ABO43617;  
 XX  
 DT 25-SEP-2003 (first entry)  
 DE  
 XX  
 XX Cadherin; CAD; extracellular domain; cell adhesion; peptidomimetic;  
 KW cadherin-mediated intercellular adhesion; tumour; cancer; angiogenesis;  
 KW central nervous system; wound healing; vasopermeability; N-cadherin;  
 KW demyelinating neurological disease; astrocyte; synaptic stability; ovary;  
 KW neurite outgrowth; spinal cord injury; macular degeneration; bladder;  
 KW melanoma; carcinoma; leukaemia; skin disorder; acute B cell leukaemia;  
 KW immune reaction; immunoglobulin; T cell generation; CAR; cyclic;  
 KW cell adhesion recognition sequence.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002168761-A1.  
 XX  
 PD 14-NOV-2002.  
 XX  
 XX 24-JAN-2001; 2001US-00769145.  
 PF  
 XX 24-JAN-2000; 2000US-00491078.  
 PR  
 XX (GOUR/) GOUR B J.  
 PA (BLAS/) BLASCHUK O W.  
 PA (ALIA/) ALI A.  
 PA (NIFF/) NI F.  
 PA (CHEN/) CHEN Z.  
 PA (MICH/) MICHAUD S D.  
 PA (WANG/) WANG S.  
 PA (HUZZ/) HU Z.  
 XX  
 XX Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;  
 PI Hu Z;  
 XX  
 XX WPI; 2003-521524/49.  
 DR  
 XX Novel cell adhesion modulating agent for modulating cadherin-mediated  
 PT intercellular adhesion, for enhancing wound healing, has three-

PT dimensional structure similar to three-dimensional structure of cyclic  
 PT peptide.  
 XX  
 XX Disclosure; Page 7; 309pp; English.  
 PS  
 CC The invention relates to a cell adhesion modulating agent which is a  
 CC peptidomimetic having a three-dimensional structure of a cyclic peptide  
 CC that comprises the sequence HAV within a cyclic peptide ring. The agent  
 CC is useful for modulating classical cadherin-mediated intercellular  
 CC adhesion, for reducing unwanted cellular adhesion in a mammal, for  
 CC enhancing the delivery of a drug to a tumour, for inhibiting the  
 CC development of cancer, for inhibiting angiogenesis, for enhancing drug  
 CC delivery to the central nervous system, for enhancing wound healing, for  
 CC enhancing the adhesion of foreign tissue implanted within a mammal, for  
 CC modulating the immune system of a mammal, for increasing  
 CC vasopermeability, for treating a demyelinating neurological disease, for  
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,  
 CC for inhibiting synaptic stability, for modulating neurite outgrowth, for  
 CC treating spinal cord injuries and for treating macular degeneration. The  
 CC cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or  
 CC leukaemia. The agent is useful for treating skin disorders, acute B cell  
 CC leukaemia, excessive immune reactions involving the humoral immune system  
 CC and generation of immunoglobulins and diseases associated with excessive  
 CC generation of T cells. This sequence represents a cadherin (CAD) cell  
 CC adhesion recognition (CAR) sequence cyclic peptide peptidomimetic of the  
 CC invention  
 XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 34; DB 7; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CHAVC 5  
 Db |||||  
 1 CHAVC 5  
 RESULT 29  
 ABO43618  
 ID ABO43618 standard; peptide; 6 AA.  
 XX  
 AC ABO43618;  
 XX  
 DT 25-SEP-2003 (first entry)  
 DE  
 XX  
 XX Cadherin; CAD; extracellular domain; cell adhesion; peptidomimetic;  
 KW cadherin-mediated intercellular adhesion; tumour; cancer; angiogenesis;  
 KW central nervous system; wound healing; vasopermeability; N-cadherin;  
 KW demyelinating neurological disease; astrocyte; synaptic stability; ovary;  
 KW neurite outgrowth; spinal cord injury; macular degeneration; bladder;  
 KW melanoma; carcinoma; leukaemia; skin disorder; acute B cell leukaemia;  
 KW immune reaction; immunoglobulin; T cell generation; CAR; cyclic;  
 KW cell adhesion recognition sequence.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002168761-A1.  
 XX  
 PD 14-NOV-2002.  
 XX  
 XX 24-JAN-2001; 2001US-00769145.  
 PF  
 XX 24-JAN-2000; 2000US-00491078.  
 PR  
 XX (GOUR/) GOUR B J.  
 PA (BLAS/) BLASCHUK O W.  
 PA (ALIA/) ALI A.  
 PA (NIFF/) NI F.  
 PA (CHEN/) CHEN Z.  
 PA (MICH/) MICHAUD S D.  
 XX  
 XX Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;  
 PI Hu Z;  
 XX  
 XX WPI; 2003-521524/49.  
 DR  
 XX Novel cell adhesion modulating agent for modulating cadherin-mediated  
 PT intercellular adhesion, for enhancing wound healing, has three-

PA (WANG/) WANG S.  
 PA (HUZZ/) HU Z.  
 XX  
 XX  
 PI Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;  
 PI Hu Z;  
 XX  
 XX WPI; 2003-521524/49.  
 DR  
 XX Novel cell adhesion modulating agent for modulating cadherin-mediated  
 PT intercellular adhesion, for enhancing wound healing, has three-  
 PT dimensional structure similar to three-dimensional structure of cyclic  
 PT peptide.  
 XX  
 XX Disclosure; Page 7; 309pp; English.  
 PS  
 XX The invention relates to a cell adhesion modulating agent which is a  
 CC peptidomimetic having a three-dimensional structure of a cyclic peptide  
 CC that comprises the sequence HAV within a cyclic peptide ring. The agent  
 CC is useful for modulating classical cadherin-mediated intercellular  
 CC adhesion, for reducing unwanted cellular adhesion in a mammal, for  
 CC enhancing the delivery of a drug to a tumour, for inhibiting the  
 CC development of cancer, for inhibiting angiogenesis, for enhancing drug  
 CC delivery to the central nervous system, for enhancing wound healing, for  
 CC enhancing the adhesion of foreign tissue implanted within a mammal, for  
 CC modulating the immune system of a mammal, for increasing  
 CC vasopermeability, for treating a demyelinating neurological disease, for  
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,  
 CC for inhibiting synaptic stability, for modulating neurite outgrowth, for  
 CC treating spinal cord injuries and for treating macular degeneration. The  
 CC cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or  
 CC leukaemia. The agent is useful for treating skin disorders, acute B cell  
 CC leukaemia, excessive immune reactions involving the humoral immune system  
 CC and generation of immunoglobulins and diseases associated with excessive  
 CC generation of T cells. This sequence represents a cadherin (CAD) cell  
 CC adhesion recognition (CAR) sequence cyclic peptide peptidomimetic of the  
 CC invention  
 XX  
 XX Sequence 6 AA;  
 SQ  
 Query Match 100.0%; Score 34; DB 7; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CHAVC 5  
 DB |||||  
 1 CHAVC 5  
 RESULT 30  
 ABO43614  
 ID ABO43614 standard; peptide; 6 AA.  
 XX  
 AC ABO43614;  
 AC  
 XX 25-SEP-2003 (first entry)  
 DT  
 XX Classical cadherin CAR sequence cyclic peptide peptidomimetic #74.  
 DE  
 XX Cadherin; CAD; extracellular domain; cell adhesion; peptidomimetic;  
 XX cadherin-mediated intercellular adhesion; tumour; cancer; angiogenesis;  
 KW central nervous system; wound healing; vasopermeability; N-cadherin;  
 KW demyelinating neurological disease; astrocyte; synaptic stability; ovary;  
 KW neurite outgrowth; spinal cord injury; macular degeneration; bladder;  
 KW melanoma; carcinoma; leukaemia; skin disorder; acute B cell leukaemia;  
 KW immune reaction; immunoglobulin; T cell generation; CAR; cyclic;  
 KW cell adhesion recognition sequence.  
 XX  
 XX Synthetic.  
 OS  
 XX US2002168761-A1.  
 PN  
 XX 14-NOV-2002.  
 PD  
 XX

PF 24-JAN-2001; 2001US-00769145.  
 XX  
 PR 24-JAN-2000; 2000US-00491078.  
 XX  
 XX (GOUR/) GOUR B J.  
 PA (BLAS/) BLASCHUK O W.  
 PA (ALIA/) ALI A.  
 PA (NIEF/) NI F.  
 PA (CHEN/) CHEN Z.  
 PA (MICH/) MICHAUD S D.  
 PA (WANG/) WANG S.  
 PA (HUZZ/) HU Z.  
 XX  
 PI Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;  
 PI Hu Z;  
 XX  
 XX WPI; 2003-521524/49.  
 DR  
 XX Novel cell adhesion modulating agent for modulating cadherin-mediated  
 PT intercellular adhesion, for enhancing wound healing, has three-  
 PT dimensional structure similar to three-dimensional structure of cyclic  
 PT peptide.  
 XX  
 XX Disclosure; Page 7; 309pp; English.  
 PS  
 XX The invention relates to a cell adhesion modulating agent which is a  
 CC peptidomimetic having a three-dimensional structure of a cyclic peptide  
 CC that comprises the sequence HAV within a cyclic peptide ring. The agent  
 CC is useful for modulating classical cadherin-mediated intercellular  
 CC adhesion, for reducing unwanted cellular adhesion in a mammal, for  
 CC enhancing the delivery of a drug to a tumour, for inhibiting the  
 CC development of cancer, for inhibiting angiogenesis, for enhancing drug  
 CC delivery to the central nervous system, for enhancing wound healing, for  
 CC enhancing the adhesion of foreign tissue implanted within a mammal, for  
 CC modulating the immune system of a mammal, for increasing  
 CC vasopermeability, for treating a demyelinating neurological disease, for  
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,  
 CC for inhibiting synaptic stability, for modulating neurite outgrowth, for  
 CC treating spinal cord injuries and for treating macular degeneration. The  
 CC cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or  
 CC leukaemia. The agent is useful for treating skin disorders, acute B cell  
 CC leukaemia, excessive immune reactions involving the humoral immune system  
 CC and generation of immunoglobulins and diseases associated with excessive  
 CC generation of T cells. This sequence represents a cadherin (CAD) cell  
 CC adhesion recognition (CAR) sequence cyclic peptide peptidomimetic of the  
 CC invention  
 XX  
 XX Sequence 6 AA;  
 SQ  
 Query Match 100.0%; Score 34; DB 7; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CHAVC 5  
 DB |||||  
 2 CHAVC 6  
 RESULT 31  
 ABO43619  
 ID ABO43619 standard; peptide; 6 AA.  
 XX  
 AC ABO43619;  
 AC  
 XX 25-SEP-2003 (first entry)  
 DT  
 XX Classical cadherin CAR sequence cyclic peptide peptidomimetic #79.  
 DE  
 XX Cadherin; CAD; extracellular domain; cell adhesion; peptidomimetic;  
 KW cadherin-mediated intercellular adhesion; tumour; cancer; angiogenesis;  
 KW central nervous system; wound healing; vasopermeability; N-cadherin;  
 KW demyelinating neurological disease; astrocyte; synaptic stability; ovary;  
 KW neurite outgrowth; spinal cord injury; macular degeneration; bladder;  
 KW immune reaction; immunoglobulin; T cell generation; CAR; cyclic;  
 KW cell adhesion recognition sequence.  
 XX  
 XX Synthetic.  
 OS  
 XX US2002168761-A1.  
 PN  
 XX 14-NOV-2002.  
 PD  
 XX

KW melanoma; carcinoma; leukaemia; skin disorder; acute B cell leukaemia;  
 KW immune reaction; immunoglobulin; T cell generation; CAR; cyclic;  
 KW cell adhesion recognition sequence.  
 XX Synthetic.  
 OS  
 XX US2002168761-A1.  
 PN  
 XX 14-NOV-2002.  
 XX  
 XX 24-JAN-2001; 2001US-00769145.  
 XX  
 XX 24-JAN-2000; 2000US-00491078.  
 XX  
 XX (GOUR/) GOUR B J.  
 PA (BLAS/) BLASCHUK O W.  
 PA (ALIA/) ALI A.  
 PA (NIFF/) NI F.  
 PA (CHEN/) CHEN Z.  
 PA (MICH/) MICHAUD S D.  
 PA (WANG/) WANG S.  
 PA (HUZZ/) HU Z.  
 XX  
 XX GOUR BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;  
 PI Hu Z;  
 PI  
 XX WPI; 2003-521524/49.  
 DR  
 XX Novel cell adhesion modulating agent for modulating cadherin-mediated  
 XX intercellular adhesion, for enhancing wound healing, has three-  
 PT dimensional structure similar to three-dimensional structure of cyclic  
 PT peptide.  
 PT  
 XX Disclosure; Page 8; 309pp; English.  
 PS  
 XX The invention relates to a cell adhesion modulating agent which is a  
 CC peptidomimetic having a three-dimensional structure of a cyclic peptide  
 CC that comprises the sequence HAV within a cyclic peptide ring. The agent  
 CC is useful for modulating classical cadherin-mediated intercellular  
 CC adhesion, for reducing unwanted cellular adhesion in a mammal, for  
 CC enhancing the delivery of a drug to a tumour, for inhibiting the  
 CC development of cancer, for inhibiting angiogenesis, for enhancing drug  
 CC delivery to the central nervous system, for enhancing wound healing, for  
 CC enhancing the adhesion of foreign tissue implanted within a mammal, for  
 CC modulating the immune system of a mammal, for increasing  
 CC vasopermeability, for treating a demyelinating neurological disease, for  
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,  
 CC for inhibiting synaptic stability, for modulating neurite outgrowth, for  
 CC treating spinal cord injuries and for treating macular degeneration. The  
 CC cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or  
 CC leukaemia. The agent is useful for treating skin disorders, acute B cell  
 CC leukaemia, excessive immune reactions involving the humoral immune system  
 CC and generation of immunoglobulins and diseases associated with excessive  
 CC generation of T cells. This sequence represents a cadherin (CAD) cell  
 CC adhesion recognition (CAR) sequence cyclic peptide peptidomimetic of the  
 CC invention  
 XX  
 XX Sequence 6 AA;  
 SQ  
 Query Match 100.0%; Score 34; DB 7; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CHAVC 5  
 Db 1 CHAVC 5  
 |||||  
 |||||  
 RESULT 32  
 ADK13619  
 ID ADK13619 standard; peptide; 6 AA.  
 XX  
 XX AC ADK13619;

XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE Cadherin-mediated cell adhesion-modulating peptidomimetic #78.  
 XX  
 XX Cell adhesion-modulating agent; cadherin-mediated cell adhesion; cancer;  
 KW angiogenesis; central nervous system; wound healing;  
 KW foreign tissue adhesion; vasopermeability;  
 KW demyelinating neurological disease; astrocyte; synaptic stability;  
 KW neurite outgrowth; spinal cord injury; macular degeneration; metastasis;  
 KW bladder; tumour; ovary; melanoma; carcinoma; leukaemia;  
 KW multiple sclerosis; cytostatic; antiangiogenic; neuroprotective;  
 KW ophthalmological; Cell adhesion-modulating peptidomimetic;  
 KW cadherin cell adhesion recognition sequence; CAR; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 XX US2004058864-A1.  
 PN  
 XX 25-MAR-2004.  
 XX  
 XX 10-APR-2003; 2003US-00412701.  
 XX  
 XX 24-JAN-2000; 2000US-00491078.  
 PR 24-JAN-2001; 2001US-00769145.  
 XX  
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
 PA  
 XX Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;  
 PI Hu Z;  
 PI  
 XX WPI; 2004-269836/25.  
 DR  
 XX New cell adhesion modulating agent, useful for treating or preventing  
 XX cancer and/or inhibiting metastasis, inhibiting angiogenesis, enhancing  
 PT wound healing, treating a demyelinating neurological disease or treating  
 PT spinal cord injuries.  
 PT  
 XX Disclosure; SEQ ID NO 85; 281pp; English.  
 PS  
 XX The invention relates to a cell adhesion-modulating agent. The invention  
 CC also relates to methods for screening a candidate compound for the  
 CC ability to modulate classical cadherin-mediated cell adhesion,  
 CC identifying a compound that modulates classical cadherin-mediated cell  
 CC adhesion, modulating classical cadherin-mediated intercellular adhesion,  
 CC reducing unwanted cellular adhesion in a mammal, enhancing the delivery  
 CC of a drug to a tumour in a mammal, inhibiting the development of a cancer  
 CC in a mammal, inhibiting angiogenesis in a mammal, enhancing wound healing in a  
 CC to the central nervous system of a mammal, increasing vasopermeability in  
 CC a mammal, enhancing adhesion of foreign tissue implanted within a mammal,  
 CC modulating the immune system of a mammal, increasing vasopermeability in  
 CC a mammal, treating a demyelinating neurological disease in a mammal,  
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,  
 CC inhibiting synaptic stability in a mammal, modulating neurite outgrowth,  
 CC treating spinal cord injuries in a mammal and treating macular  
 CC degeneration in a mammal. The compounds are useful for inhibiting or  
 CC enhancing cadherin-mediated cell adhesion. The cell adhesion modulating  
 CC agents are useful for inhibiting the development of cancer, e.g. treating  
 CC or preventing cancer and/or inhibiting metastasis. The cancer is a  
 CC bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The  
 CC agents are also useful in inhibiting angiogenesis, for enhancing the  
 CC delivery of a drug to a tumour in a mammal, for enhancing wound healing  
 CC to the central nervous system of a mammal, for enhancing wound healing in  
 CC a mammal, for enhancing adhesion of foreign tissue implanted within a  
 CC mammal, for modulating the immune system of a mammal, for treating a  
 CC demyelinating neurological disease (such as multiple sclerosis) in a  
 CC mammal, for inhibiting synaptic stability in a mammal, for modulating  
 CC neurite outgrowth, for treating spinal cord injuries in a mammal and for  
 CC treating macular degeneration in a mammal. This sequence represents a  
 CC cadherin-mediated cell adhesion-modulating peptidomimetic, comprising a  
 CC classical cadherin cell adhesion recognition (CAR) sequence.  
 XX  
 XX Sequence 6 AA;  
 SQ

Query Match 100.0%; Score 34; DB 8; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
 DB 2 CHAVC 6  
 |||||  
 |||||

RESULT 33  
 ADK13622  
 ID ADK13622 standard; peptide; 6 AA.  
 XX  
 AC ADK13622;  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE Cadherin-mediated cell adhesion-modulating peptidomimetic #81.  
 XX  
 KW Cell adhesion-modulating agent; cadherin-mediated cell adhesion; cancer;  
 KW angiogenesis; central nervous system; wound healing;  
 KW foreign tissue adhesion; vasopermeability;  
 KW demyelinating neurological disease; astrocyte; synaptic stability;  
 KW neurite outgrowth; spinal cord injury; macular degeneration; metastasis;  
 KW bladder; tumour; ovary; melanoma; carcinoma; leukaemia;  
 KW multiple sclerosis; cystostatic; antiangiogenic; neuroprotective;  
 KW ophthalmological; Cell adhesion-modulating peptidomimetic;  
 KW cadherin cell adhesion recognition sequence; CAR; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 PN US2004058864-A1.  
 XX  
 PD 25-MAR-2004.  
 XX  
 PF 10-APR-2003; 2003US-00412701.  
 XX  
 PR 24-JAN-2000; 2000US-00491078.  
 PR 24-JAN-2001; 2001US-00769145.  
 XX  
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX  
 PI Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;  
 PI Hu Z;  
 XX  
 DR WPI; 2004-268836/25.  
 XX  
 PS New cell adhesion modulating agent, useful for treating or preventing  
 cancer and/or inhibiting metastasis, inhibiting angiogenesis, enhancing  
 wound healing, treating a demyelinating neurological disease or treating  
 spinal cord injuries.  
 XX  
 PS Disclosure; SEQ ID NO 88; 281pp; English.  
 XX  
 CC The invention relates to a cell adhesion-modulating agent. The invention  
 also relates to methods for screening a candidate compound for the  
 ability to modulate classical cadherin-mediated cell adhesion,  
 identifying a compound that modulates classical cadherin-mediated cell  
 adhesion, modulating classical cadherin-mediated intercellular adhesion,  
 reducing unwanted cellular adhesion in a mammal, enhancing the delivery  
 of a drug to a tumour in a mammal, inhibiting the development of a cancer  
 in a mammal, inhibiting angiogenesis in a mammal, enhancing drug delivery  
 to the central nervous system of a mammal, enhancing wound healing in a  
 mammal, enhancing adhesion of foreign tissue implanted within a mammal,  
 modulating the immune system of a mammal, increasing vasopermeability in  
 a mammal, treating a demyelinating neurological disease in a mammal,  
 facilitating migration of an N-cadherin-expressing cell on astrocytes,  
 inhibiting synaptic stability in a mammal, modulating neurite outgrowth,  
 treating spinal cord injuries in a mammal and treating macular  
 degeneration in a mammal. The compounds are useful for inhibiting or  
 enhancing cadherin-mediated cell adhesion. The cell adhesion modulating  
 agents are useful for inhibiting the development of cancer, e.g. treating

or preventing cancer and/or inhibiting metastasis. The cancer is a  
 bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The  
 agents are also useful in inhibiting angiogenesis, for enhancing the  
 delivery of a drug to a tumour in a mammal, for enhancing wound healing in  
 to the central nervous system of a mammal, for enhancing drug delivery  
 a mammal, for enhancing adhesion of foreign tissue implanted within a  
 mammal, for modulating the immune system of a mammal, for treating a  
 demyelinating neurological disease (such as multiple sclerosis) in a  
 mammal, for inhibiting synaptic stability in a mammal, for modulating  
 neurite outgrowth, for treating spinal cord injuries in a mammal and for  
 treating macular degeneration in a mammal. This sequence represents a  
 cadherin-mediated cell adhesion-modulating peptidomimetic, comprising a  
 classical cadherin cell adhesion recognition (CAR) sequence.

Sequence 6 AA;  
 Query Match 100.0%; Score 34; DB 8; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
 DB 1 CHAVC 5  
 |||||  
 |||||

RESULT 34  
 ADK13623  
 ID ADK13623 standard; peptide; 6 AA.  
 XX  
 AC ADK13623;  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE Cadherin-mediated cell adhesion-modulating peptidomimetic #82.  
 XX  
 KW Cell adhesion-modulating agent; cadherin-mediated cell adhesion; cancer;  
 KW angiogenesis; central nervous system; wound healing;  
 KW foreign tissue adhesion; vasopermeability;  
 KW demyelinating neurological disease; astrocyte; synaptic stability;  
 KW neurite outgrowth; spinal cord injury; macular degeneration; metastasis;  
 KW bladder; tumour; ovary; melanoma; carcinoma; leukaemia;  
 KW multiple sclerosis; cystostatic; antiangiogenic; neuroprotective;  
 KW ophthalmological; Cell adhesion-modulating peptidomimetic;  
 KW cadherin cell adhesion recognition sequence; CAR; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 PN US2004058864-A1.  
 XX  
 PD 25-MAR-2004.  
 XX  
 PF 10-APR-2003; 2003US-00412701.  
 XX  
 PR 24-JAN-2000; 2000US-00491078.  
 PR 24-JAN-2001; 2001US-00769145.  
 XX  
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX  
 PI Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;  
 PI Hu Z;  
 XX  
 DR WPI; 2004-268836/25.  
 XX  
 PS New cell adhesion modulating agent, useful for treating or preventing  
 cancer and/or inhibiting metastasis, inhibiting angiogenesis, enhancing  
 wound healing, treating a demyelinating neurological disease or treating  
 spinal cord injuries.  
 XX  
 PS Disclosure; SEQ ID NO 89; 281pp; English.  
 XX  
 CC The invention relates to a cell adhesion-modulating agent. The invention  
 also relates to methods for screening a candidate compound for the  
 ability to modulate classical cadherin-mediated cell adhesion,  
 identifying a compound that modulates classical cadherin-mediated cell  
 adhesion, modulating classical cadherin-mediated intercellular adhesion,  
 reducing unwanted cellular adhesion in a mammal, enhancing the delivery  
 of a drug to a tumour in a mammal, inhibiting the development of a cancer  
 in a mammal, inhibiting angiogenesis in a mammal, enhancing drug delivery  
 to the central nervous system of a mammal, enhancing wound healing in a  
 mammal, enhancing adhesion of foreign tissue implanted within a mammal,  
 modulating the immune system of a mammal, increasing vasopermeability in  
 a mammal, treating a demyelinating neurological disease in a mammal,  
 facilitating migration of an N-cadherin-expressing cell on astrocytes,  
 inhibiting synaptic stability in a mammal, modulating neurite outgrowth,  
 treating spinal cord injuries in a mammal and treating macular  
 degeneration in a mammal. The compounds are useful for inhibiting or  
 enhancing cadherin-mediated cell adhesion. The cell adhesion modulating  
 agents are useful for inhibiting the development of cancer, e.g. treating

CC identifying a compound that modulates classical cadherin-mediated cell  
 CC adhesion, modulating classical cadherin-mediated intercellular adhesion,  
 CC reducing unwanted cellular adhesion in a mammal, enhancing the delivery  
 CC of a drug to a tumour in a mammal, inhibiting the development of a cancer  
 CC in a mammal, inhibiting angiogenesis in a mammal, enhancing drug delivery  
 CC to the central nervous system of a mammal, enhancing wound healing in a  
 CC mammal, enhancing adhesion of foreign tissue implanted within a mammal,  
 CC modulating the immune system of a mammal, increasing vasopermeability in  
 CC a mammal, treating a demyelinating neurological disease in a mammal,  
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,  
 CC inhibiting synaptic stability in a mammal, modulating neurite outgrowth,  
 CC treating spinal cord injuries in a mammal and treating macular  
 CC degeneration in a mammal. The compounds are useful for inhibiting or  
 CC enhancing cadherin-mediated cell adhesion. The cell adhesion modulating  
 CC agents are useful for inhibiting the development of cancer, e.g. treating  
 CC or preventing cancer and/or inhibiting metastasis. The cancer is a  
 CC bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The  
 CC agents are also useful in inhibiting angiogenesis, for enhancing the  
 CC delivery of a drug to a tumour in a mammal, for enhancing wound healing in  
 CC to the central nervous system of a mammal, for enhancing wound healing in  
 CC a mammal, for enhancing adhesion of foreign tissue implanted within a  
 CC mammal, for modulating the immune system of a mammal, for treating a  
 CC demyelinating neurological disease (such as multiple sclerosis) in a  
 CC mammal, for inhibiting synaptic stability in a mammal, for modulating  
 CC neurite outgrowth, for treating spinal cord injuries in a mammal and for  
 CC treating macular degeneration in a mammal. This sequence represents a  
 CC cadherin-mediated cell adhesion-modulating peptidomimetic, comprising a  
 CC classical cadherin cell adhesion recognition (CAR) sequence.

XX Sequence 6 AA;

Query Match 100.0%; Score 34; DB 8; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 1 CHAVC 5

RESULT 35

ADK13615  
 ID ADK13615 standard; peptide; 6 AA.

XX AC ADK13615;

XX DT 17-JUN-2004 (first entry)

XX DE Cadherin-mediated cell adhesion-modulating peptidomimetic #74.

XX Cell adhesion-modulating agent; cadherin-mediated cell adhesion; cancer;  
 KW angiogenesis; central nervous system; wound healing;  
 KW foreign tissue adhesion; vasopermeability;  
 KW demyelinating neurological disease; astrocyte; synaptic stability;  
 KW neurite outgrowth; spinal cord injury; macular degeneration; metastasis;  
 KW bladder; tumour; ovary; melanoma; carcinoma; leukaemia;  
 KW multiple sclerosis; cytostatic; antiangiogenic; neuroprotective;  
 KW ophthalmological; Cell adhesion-modulating peptidomimetic;  
 KW cadherin cell adhesion recognition sequence; CAR; cyclic.

XX Synthetic.

XX OS US2004058864-A1.

XX PN 25-MAR-2004.

XX PD 10-APR-2003; 2003US-00412701.

XX PF 24-JAN-2000; 2000US-00491078.

XX PR 24-JAN-2001; 2001US-00769145.

XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.

XX

PI Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;  
 PI Hu Z;

XX WPI; 2004-268836/25.

DR New cell adhesion modulating agent, useful for treating or preventing  
 PT cancer and/or inhibiting metastasis, inhibiting angiogenesis, enhancing  
 PT wound healing, treating a demyelinating neurological disease or treating  
 PT spinal cord injuries.

XX Claim 15; SEQ ID NO 81; 281pp; English.

XX The invention relates to a cell adhesion-modulating agent. The invention  
 CC also relates to methods for screening a candidate compound for the  
 CC ability to modulate classical cadherin-mediated cell adhesion,  
 CC identifying a compound that modulates classical cadherin-mediated cell  
 CC adhesion, modulating classical cadherin-mediated intercellular adhesion,  
 CC reducing unwanted cellular adhesion in a mammal, enhancing the delivery  
 CC of a drug to a tumour in a mammal, inhibiting the development of a cancer  
 CC in a mammal, inhibiting angiogenesis in a mammal, enhancing drug delivery  
 CC to the central nervous system of a mammal, enhancing wound healing in a  
 CC mammal, enhancing adhesion of foreign tissue implanted within a mammal,  
 CC modulating the immune system of a mammal, increasing vasopermeability in  
 CC a mammal, treating a demyelinating neurological disease in a mammal,  
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,  
 CC inhibiting synaptic stability in a mammal, modulating neurite outgrowth,  
 CC treating spinal cord injuries in a mammal and treating macular  
 CC degeneration in a mammal. The compounds are useful for inhibiting or  
 CC enhancing cadherin-mediated cell adhesion. The cell adhesion modulating  
 CC agents are useful for inhibiting the development of cancer, e.g. treating  
 CC or preventing cancer and/or inhibiting metastasis. The cancer is a  
 CC bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The  
 CC agents are also useful in inhibiting angiogenesis, for enhancing the  
 CC delivery of a drug to a tumour in a mammal, for enhancing wound healing in  
 CC to the central nervous system of a mammal, for enhancing wound healing in  
 CC a mammal, for enhancing adhesion of foreign tissue implanted within a  
 CC mammal, for modulating the immune system of a mammal, for treating a  
 CC demyelinating neurological disease (such as multiple sclerosis) in a  
 CC mammal, for inhibiting synaptic stability in a mammal, for modulating  
 CC neurite outgrowth, for treating spinal cord injuries in a mammal and for  
 CC treating macular degeneration in a mammal. This sequence represents a  
 CC cadherin-mediated cell adhesion-modulating peptidomimetic, comprising a  
 CC classical cadherin cell adhesion recognition (CAR) sequence.

XX Sequence 6 AA;

Query Match 100.0%; Score 34; DB 8; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 1 CHAVC 5

RESULT 36

ADK13624  
 ID ADK13624 standard; peptide; 6 AA.

XX AC ADK13624;

XX DT 17-JUN-2004 (first entry)

XX DE Cadherin-mediated cell adhesion-modulating peptidomimetic #83.

XX Cell adhesion-modulating agent; cadherin-mediated cell adhesion; cancer;  
 KW angiogenesis; central nervous system; wound healing;  
 KW foreign tissue adhesion; vasopermeability;  
 KW demyelinating neurological disease; astrocyte; synaptic stability;  
 KW neurite outgrowth; spinal cord injury; macular degeneration; metastasis;  
 KW bladder; tumour; ovary; melanoma; carcinoma; leukaemia;  
 KW multiple sclerosis; cytostatic; antiangiogenic; neuroprotective;  
 KW ophthalmological; Cell adhesion-modulating peptidomimetic;



KW cadherin cell adhesion recognition sequence; CAR; cyclic.  
 XX Synthetic.  
 OS  
 PN US2004058864-A1.  
 XX  
 XX 25-MAR-2004.  
 PD  
 XX  
 XX 10-APR-2003; 2003US-00412701.  
 PF  
 XX 24-JAN-2000; 2000US-00491078.  
 PR  
 XX 24-JAN-2001; 2001US-00769145.  
 XX  
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
 PA  
 XX Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;  
 PI Hu Z;  
 PI WPI; 2004-268836/25.  
 DR  
 XX New cell adhesion modulating agent, useful for treating or preventing  
 PT cancer and/or inhibiting metastasis, inhibiting angiogenesis, enhancing  
 PT wound healing, treating a demyelinating neurological disease or treating  
 PT spinal cord injuries.  
 XX  
 XX Disclosure; SEQ ID NO 90; 281pp; English.  
 PS  
 XX The invention relates to a cell adhesion-modulating agent. The invention  
 CC also relates to methods for screening a candidate compound for the  
 CC ability to modulate classical cadherin-mediated cell adhesion.  
 CC identifying a compound that modulates classical cadherin-mediated cell  
 CC adhesion, modulating classical cadherin-mediated intercellular adhesion,  
 CC reducing unwanted cellular adhesion in a mammal, enhancing the delivery  
 CC of a drug to a tumour in a mammal, inhibiting the development of a cancer  
 CC in a mammal, inhibiting angiogenesis in a mammal, enhancing drug delivery  
 CC to the central nervous system of a mammal, enhancing wound healing in a  
 CC mammal, enhancing adhesion of foreign tissue implanted within a mammal,  
 CC modulating the immune system of a mammal, increasing vasopermeability in  
 CC a mammal, treating a demyelinating neurological disease in a mammal,  
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,  
 CC inhibiting synaptic stability in a mammal, modulating neurite outgrowth,  
 CC treating spinal cord injuries in a mammal and treating macular  
 CC degeneration in a mammal. The compounds are useful for inhibiting or  
 CC enhancing cadherin-mediated cell adhesion. The cell adhesion modulating  
 CC agents are useful for inhibiting the development of cancer, e.g. treating  
 CC or preventing cancer and/or inhibiting metastasis. The cancer is a  
 CC bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The  
 CC agents are also useful in inhibiting angiogenesis, for enhancing the  
 CC delivery of a drug to a tumour in a mammal, for enhancing drug delivery  
 CC to the central nervous system of a mammal, for enhancing wound healing in  
 CC a mammal, for enhancing adhesion of foreign tissue implanted within a  
 CC mammal, for modulating the immune system of a mammal, for treating a  
 CC demyelinating neurological disease (such as multiple sclerosis) in a  
 CC mammal, for inhibiting synaptic stability in a mammal, for modulating  
 CC neurite outgrowth, for treating spinal cord injuries in a mammal and for  
 CC treating macular degeneration in a mammal. This sequence represents a  
 CC cadherin-mediated cell adhesion-modulating peptidomimetic, comprising a  
 CC classical cadherin cell adhesion recognition (CAR) sequence.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 34; DB 8; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CHAVC 5  
 |||||  
 Db 1 CHAVC 5  
 RESULT 37  
 ADK13618  
 ID ADK13618 standard; peptide; 6 AA.

XX  
 AC  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 XX Cadherin-mediated cell adhesion-modulating peptidomimetic #77.  
 DE  
 XX  
 XX Cell adhesion-modulating agent; cadherin-mediated cell adhesion; cancer;  
 KW angiogenesis; central nervous system; wound healing;  
 KW foreign tissue adhesion; vasopermeability;  
 KW demyelinating neurological disease; astrocyte; synaptic stability;  
 KW neurite outgrowth; spinal cord injury; macular degeneration; metastasis;  
 KW bladder; tumour; ovary; melanoma; carcinoma; leukaemia;  
 KW multiple sclerosis; cytostatic; antiangiogenic; neuroprotective;  
 KW ophthalmological; cell adhesion-modulating peptidomimetic;  
 KW cadherin cell adhesion recognition sequence; CAR; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 XX US2004058864-A1.  
 PN  
 XX 25-MAR-2004.  
 PD  
 XX  
 XX 10-APR-2003; 2003US-00412701.  
 PF  
 XX 24-JAN-2000; 2000US-00491078.  
 PR  
 XX 24-JAN-2001; 2001US-00769145.  
 XX  
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
 PA  
 XX Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;  
 PI Hu Z;  
 PI WPI; 2004-268836/25.  
 DR  
 XX New cell adhesion modulating agent, useful for treating or preventing  
 PT cancer and/or inhibiting metastasis, inhibiting angiogenesis, enhancing  
 PT wound healing, treating a demyelinating neurological disease or treating  
 PT spinal cord injuries.  
 XX  
 XX Disclosure; SEQ ID NO 84; 281pp; English.  
 PS  
 XX The invention relates to a cell adhesion-modulating agent. The invention  
 CC also relates to methods for screening a candidate compound for the  
 CC ability to modulate classical cadherin-mediated cell adhesion,  
 CC identifying a compound that modulates classical cadherin-mediated cell  
 CC adhesion, modulating classical cadherin-mediated intercellular adhesion,  
 CC reducing unwanted cellular adhesion in a mammal, enhancing the delivery  
 CC of a drug to a tumour in a mammal, inhibiting the development of a cancer  
 CC in a mammal, inhibiting angiogenesis in a mammal, enhancing drug delivery  
 CC to the central nervous system of a mammal, enhancing wound healing in a  
 CC mammal, enhancing adhesion of foreign tissue implanted within a mammal,  
 CC modulating the immune system of a mammal, increasing vasopermeability in  
 CC a mammal, treating a demyelinating neurological disease in a mammal,  
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,  
 CC inhibiting synaptic stability in a mammal, modulating neurite outgrowth,  
 CC treating spinal cord injuries in a mammal and treating macular  
 CC degeneration in a mammal. The compounds are useful for inhibiting or  
 CC enhancing cadherin-mediated cell adhesion. The cell adhesion modulating  
 CC agents are useful for inhibiting the development of cancer, e.g. treating  
 CC or preventing cancer and/or inhibiting metastasis. The cancer is a  
 CC bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The  
 CC agents are also useful in inhibiting angiogenesis, for enhancing the  
 CC delivery of a drug to a tumour in a mammal, for enhancing drug delivery  
 CC to the central nervous system of a mammal, for enhancing wound healing in  
 CC a mammal, for enhancing adhesion of foreign tissue implanted within a  
 CC mammal, for modulating the immune system of a mammal, for treating a  
 CC demyelinating neurological disease (such as multiple sclerosis) in a  
 CC mammal, for inhibiting synaptic stability in a mammal, for modulating  
 CC neurite outgrowth, for treating spinal cord injuries in a mammal and for  
 CC treating macular degeneration in a mammal. This sequence represents a  
 CC cadherin-mediated cell adhesion-modulating peptidomimetic, comprising a  
 CC classical cadherin cell adhesion recognition (CAR) sequence.



```

XX SQ Sequence 6 AA;
Query Match 100.0%; Score 34; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CHAVC 5
Db 1 CHAVC 5

RESULT 38
AAG65447
ID AAG65447 standard; peptide; 7 AA.
XX AC AAG65447;
XX 30-NOV-2001 (first entry)
XX DE Cyclic peptide with classical cadherin CAR sequence.
XX KW Cell adhesion; imidazole; peptidomimetic; cadherin; angiogenesis; CAR;
XX KW cytosolic; vulnarary; immunomodulator; vasotropic; neuroprotective;
XX KW cerebroprotective; muscular; cyclic.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 1 /note= "putative N-terminal acetylation or
FT FT alkoxybenzylation"
FT Modified-site 7 /note= "putative C-terminal amide or ester"
FT FT
FT WO200153331-A2.
XX PN
XX PD 26-JUL-2001.
XX PF 24-JAN-2001; 2001WO-US002508.
XX PR 24-JAN-2000; 2000US-00491078.
XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX PI Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;
XX PI Hu Z;
XX DR WPI; 2001-549899/61.
XX PT Cell adhesion modulating agent used for enhancing delivery of drug to
XX PT tumor comprises imidazole compounds.
XX PS Example; Page 413; 436pp; English.
XX The invention relates to cell adhesion modulating agents that comprise
XX imidazole compounds of specified formulae that are peptidomimetics of
XX cyclic peptides. The peptidomimetics have a structure similar to that of
XX a cyclic peptide that comprises a cadherin cell recognition sequence HAV.
XX The agents are used for modulating classical cadherin mediated
XX intercellular adhesion, reducing unwanted cellular adhesion, enhancing
XX delivery of a drug to a tumor, inhibiting development of cancer,
XX inhibiting angiogenesis, enhancing drug delivery to the CNS, enhancing
XX wound healing, modulating the immune system, increasing vasopermeability,
XX treating demyelinating disease, facilitating migration of an N-cadherin
XX expressing cell on astrocytes, inhibiting synaptic stability, modulating
XX neurite outgrowth, and treating spinal cord injuries and macular
XX degeneration. The present sequence represents a cyclic peptide with
XX classical cadherin cell adhesion recognition (CAR) sequence
XX SQ Sequence 7 AA;
Query Match 100.0%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CHAVC 5
Db 1 CHAVC 5

RESULT 39
AAG65446
ID AAG65446 standard; peptide; 7 AA.
XX AC AAG65446;
XX 30-NOV-2001 (first entry)
XX DE Cyclic peptide with classical cadherin CAR sequence.
XX KW Cell adhesion; imidazole; peptidomimetic; cadherin; angiogenesis; CAR;
XX KW cytosolic; vulnarary; immunomodulator; vasotropic; neuroprotective;
XX KW cerebroprotective; muscular; cyclic.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 1 /note= "putative N-terminal acetylation or
FT FT alkoxybenzylation"
FT Modified-site 7 /note= "putative C-terminal amide or ester"
FT FT
FT WO200153331-A2.
XX PN
XX PD 26-JUL-2001.
XX PF 24-JAN-2001; 2001WO-US002508.
XX PR 24-JAN-2000; 2000US-00491078.
XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX PI Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;
XX PI Hu Z;
XX DR WPI; 2001-549899/61.
XX PT Cell adhesion modulating agent used for enhancing delivery of drug to
XX PT tumor comprises imidazole compounds.
XX PS Example; Page 413; 436pp; English.
XX The invention relates to cell adhesion modulating agents that comprise
XX imidazole compounds of specified formulae that are peptidomimetics of
XX cyclic peptides. The peptidomimetics have a structure similar to that of
XX a cyclic peptide that comprises a cadherin cell recognition sequence HAV.
XX The agents are used for modulating classical cadherin mediated
XX intercellular adhesion, reducing unwanted cellular adhesion, enhancing
XX delivery of a drug to a tumor, inhibiting development of cancer,
XX inhibiting angiogenesis, enhancing drug delivery to the CNS, enhancing
XX wound healing, modulating the immune system, increasing vasopermeability,
XX treating demyelinating disease, facilitating migration of an N-cadherin
XX expressing cell on astrocytes, inhibiting synaptic stability, modulating
XX neurite outgrowth, and treating spinal cord injuries and macular
XX degeneration. The present sequence represents a cyclic peptide with
XX classical cadherin cell adhesion recognition (CAR) sequence
XX SQ Sequence 7 AA;
Query Match 100.0%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CHAVC 5
Db 1 CHAVC 5

```

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Db          |||||
            1 CHAVC 5

RESULT 40
AAM47556
ID AAM47556 standard; peptide; 7 AA.
XX
AC AAM47556;
XX
DT 12-FEB-2002 (first entry)
XX
DE Cyclic peptide endothelial cell adhesion modulator #17.
XX
KW Cadherin; cytostatic; gynecological; endometriosis;
KW endothelial cell adhesion; angiogenesis; vasopermeability; tumour;
KW cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "Linked to residue 7 to form a cyclic peptide, N-
FT terminal acetyl or N-terminal CH3-SO2 group"
FT Modified-site 7
FT /note= "linked to residue 1 to form a cyclic peptide, C-
FT terminal amide"
XX
XX WO200177146-A2.
XX
XX 18-OCT-2001.
XX
XX 09-APR-2001; 2001WO-US011669.
XX
XX 07-APR-2000; 2000US-00544782.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Blaschuk OW, Gour BJ, Farookhi R, Ali A;
XX WPI; 2002-049129/06.
XX
XX Modulating endothelial cell adhesion for inhibiting development of
XX endometriosis, increasing blood flow to tumor in a mammal, by contacting
XX cell with a cyclic peptide having cadherin cell adhesion recognition
XX sequence.
XX
XX Claim 6; Page 64; 139pp; English.
XX
XX The present invention relates to a method for modulating endothelial cell
XX adhesion. The method comprises contacting an endothelial cell with a
XX modulating peptide comprising a cadherin cell adhesion recognition
XX sequence (His Ala Val) within a cyclic peptide ring. The method is useful
XX for inhibiting angiogenesis, increasing vasopermeability, increasing
XX blood flow to a tumour, disrupting neovasculture and inhibiting the
XX development of endometriosis in a mammal. The modulating peptide reduces
XX unwanted endothelial adhesion occurring between tumour cells, tumour
XX cells and normal cells, normal cells as a result of surgery, injury,
XX chemotherapy, disease and inflammation. The present sequence is one such
XX modulating peptide
XX
XX Sequence 7 AA;
XX
Query Match 100.0%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy' 1 CHAVC 5
      |||||
      1 CHAVC 5

Db
      |||||
      1 CHAVC 5

RESULT 41

```

```

AAM47563
ID AAM47563 standard; peptide; 7 AA.
XX
XX AAM47563;
XX
DT 12-FEB-2002 (first entry)
XX
DE Cyclic peptide endothelial cell adhesion modulator #39.
XX
KW Cadherin; cytostatic; gynecological; endometriosis;
KW endothelial cell adhesion; angiogenesis; vasopermeability; tumour;
KW cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "Linked to residue 7 to form a cyclic peptide, N-
FT terminal CH3-SO2 group"
FT Modified-site 7
FT /note= "Linked to residue 1 to form a cyclic peptide, C-
FT terminal amide"
XX
XX WO200177146-A2.
XX
XX 18-OCT-2001.
XX
XX 09-APR-2001; 2001WO-US011669.
XX
XX 07-APR-2000; 2000US-00544782.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Blaschuk OW, Gour BJ, Farookhi R, Ali A;
XX WPI; 2002-049129/06.
XX
XX Modulating endothelial cell adhesion for inhibiting development of
XX endometriosis, increasing blood flow to tumor in a mammal, by contacting
XX cell with a cyclic peptide having cadherin cell adhesion recognition
XX sequence.
XX
XX Disclosure; Page 5; 139pp; English.
XX
XX The present invention relates to a method for modulating endothelial cell
XX adhesion. The method comprises contacting an endothelial cell with a
XX modulating peptide comprising a cadherin cell adhesion recognition
XX sequence (His Ala Val) within a cyclic peptide ring. The method is useful
XX for inhibiting angiogenesis, increasing vasopermeability, increasing
XX blood flow to a tumour, disrupting neovasculture and inhibiting the
XX development of endometriosis in a mammal. The modulating peptide reduces
XX unwanted endothelial adhesion occurring between tumour cells, tumour
XX cells and normal cells, normal cells as a result of surgery, injury,
XX chemotherapy, disease and inflammation. The present sequence is one such
XX modulating peptide
XX
XX Sequence 7 AA;
XX
Query Match 100.0%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
     |||||
     3 CHAVC 7

Db
     |||||
     3 CHAVC 7

RESULT 42
AAM47557
ID AAM47557 standard; peptide; 7 AA.
XX
XX AAM47557;
XX

```

DT 12-FEB-2002 (first entry)  
 DE Cyclic peptide endothelial cell adhesion modulator #18.  
 XX Cadherin; cytostatic; gynecological; endometriosis;  
 KW endothelial cell adhesion; angiogenesis; vasopermeability; tumour;  
 KW cyclic.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FT Modified-site 1 /note= "Linked to residue 7 to form a cyclic peptide, N-  
 FT terminal acetyl or N-terminal CH3-SO2 group"  
 FT Modified-site 7 /note= "Linked to residue 1 to form a cyclic peptide, C-  
 FT terminal amide"  
 FT WO200177146-A2.  
 XX 18-OCT-2001.  
 XX 09-APR-2001; 2001WO-US011669.  
 XX 07-APR-2000; 2000US-00544782.  
 XX (UYMC-) UNIV MCGILL.  
 XX Blaschuk OW, Gour BJ, Farookhi R, Ali A;  
 XX WPI; 2002-049129/06.  
 XX Modulating endothelial cell adhesion for inhibiting development of  
 PT endometriosis, increasing blood flow to tumor in a mammal, by contacting  
 FT cell with a cyclic peptide having cadherin cell adhesion recognition  
 FT sequence.  
 XX Claim 6; Page 64; 139pp; English.  
 XX The present invention relates to a method for modulating endothelial cell  
 CC adhesion. The method comprises contacting an endothelial cell with a  
 CC modulating peptide comprising a cadherin cell adhesion recognition  
 CC sequence (His Ala Val) within a cyclic peptide ring. The method is useful  
 CC for inhibiting angiogenesis, increasing vasopermeability, increasing  
 CC blood flow to a tumour, disrupting neovasculation and inhibiting the  
 CC development of endometriosis in a mammal. The modulating peptide reduces  
 CC unwanted endothelial adhesion occurring between tumour cells, tumour  
 CC cells and normal cells, normal cells as a result of surgery, injury,  
 CC chemotherapy, disease and inflammation. The present sequence is one such  
 CC modulating peptide  
 XX Sequence 7 AA;  
 SQ Query Match 100.0%; Score 34; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CHAVC 5  
 Db 2 CHAVC 6  
 RESULT 43  
 ABO43616  
 ID ABO43616 standard; peptide; 7 AA.  
 XX ABO43616;  
 AC ABO43616;  
 XX 25-SEP-2003 (first entry)  
 DT Classical cadherin CAR sequence cyclic peptide peptidomimetic #76.  
 DE Classical cadherin CAR sequence cyclic peptide peptidomimetic #76.  
 XX Cadherin; CAD; extracellular domain; cell adhesion; peptidomimetic;  
 KW

KW cadherin-mediated intercellular adhesion; tumour; cancer; angiogenesis;  
 KW central nervous system; wound healing; vasopermeability; N-cadherin;  
 KW demyelinating neurological disease; astrocyte; synaptic stability; ovary;  
 KW neurite outgrowth; spinal cord injury; macular degeneration; bladder;  
 KW melanoma; carcinoma; leukaemia; skin disorder; acute B cell leukaemia;  
 KW immune reaction; immunoglobulin; T cell generation; CAR; cyclic;  
 KW cell adhesion recognition sequence.  
 XX Synthetic.  
 XX OS US2002168761-A1.  
 XX PN 14-NOV-2002.  
 XX PD 24-JAN-2001; 2001US-00769145.  
 XX PF 24-JAN-2000; 2000US-00491078.  
 XX PR (GOUR/) GOUR B J.  
 XX (BLAS/) BLASCHUK O W.  
 XX (ALIA/) ALI A.  
 XX (NIFP/) NI F.  
 XX (CHEN/) CHEN Z.  
 XX (MICH/) MICHAUD S D.  
 XX (WANG/) WANG S.  
 XX (HUZZ/) HU Z.  
 XX Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;  
 PI Hu Z;  
 XX WPI; 2003-521524/49.  
 XX Novel cell adhesion modulating agent for modulating cadherin-mediated  
 PT intercellular adhesion, for enhancing wound healing, has three-  
 PT dimensional structure similar to three-dimensional structure of cyclic  
 PT peptide.  
 XX Disclosure; Page 7; 309pp; English.  
 XX The invention relates to a cell adhesion modulating agent which is a  
 CC peptidomimetic having a three-dimensional structure of a cyclic peptide  
 CC that comprises the sequence HAV within a cyclic peptide ring. The agent  
 CC is useful for modulating classical cadherin-mediated intercellular  
 CC adhesion, for reducing unwanted cellular adhesion in a mammal, for  
 CC enhancing the delivery of a drug to a tumour, for inhibiting the  
 CC development of cancer, for inhibiting angiogenesis, for enhancing drug  
 CC delivery to the central nervous system, for enhancing wound healing, for  
 CC enhancing the adhesion of foreign tissue implanted within a mammal, for  
 CC modulating the immune system of a mammal, for increasing  
 CC vasopermeability, for treating a demyelinating neurological disease, for  
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,  
 CC for inhibiting synaptic stability, for modulating neurite outgrowth, for  
 CC treating spinal cord injuries and for treating macular degeneration. The  
 CC cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or  
 CC leukaemia. The agent is useful for treating skin disorders, acute B cell  
 CC leukaemia, excessive immune reactions involving the humoral immune system  
 CC and generation of immunoglobulins and diseases associated with excessive  
 CC generation of T cells. This sequence represents a cadherin (CAD) cell  
 CC adhesion recognition (CAR) sequence cyclic peptide peptidomimetic of the  
 CC invention  
 XX Sequence 7 AA;  
 SQ Query Match 100.0%; Score 34; DB 7; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CHAVC 5  
 Db 2 CHAVC 6  
 RESULT 44



CC bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The  
 CC agents are also useful in inhibiting angiogenesis, for enhancing the  
 CC delivery of a drug to a tumour in a mammal, for enhancing drug delivery  
 CC to the central nervous system of a mammal, for enhancing wound healing in  
 CC a mammal, for enhancing adhesion of foreign tissue implanted within a  
 CC mammal, for modulating the immune system of a mammal, for treating a  
 CC demyelinating neurological disease (such as multiple sclerosis) in a  
 CC mammal, for inhibiting synaptic stability in a mammal, for modulating  
 CC neurite outgrowth, for treating spinal cord injuries in a mammal and for  
 CC treating macular degeneration in a mammal. This sequence represents a  
 CC cadherin-mediated cell adhesion-modulating peptidomimetic, comprising a  
 CC classical cadherin cell adhesion recognition (CAR) sequence.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 100.0%; Score 34; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CHAVC 5  
 DB 1 CHAVC 5  
 |||||  
 RESULT 46  
 ADK13621  
 ID ADK13621 standard; peptide; 7 AA.  
 XX  
 AC ADK13621;  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE Cadherin-mediated cell adhesion-modulating peptidomimetic #80.  
 XX  
 KW Cell adhesion-modulating agent; cadherin-mediated cell adhesion; cancer;  
 KW angiogenesis; central nervous system; wound healing;  
 KW foreign tissue adhesion; vasopermeability;  
 KW demyelinating neurological disease; astrocyte; synaptic stability;  
 KW neurite outgrowth; spinal cord injury; macular degeneration; metastasis;  
 KW bladder; tumour; ovary; melanoma; carcinoma; leukaemia;  
 KW multiple sclerosis; cytostatic; antiangiogenic; neuroprotective;  
 KW ophthalmological; Cell adhesion-modulating peptidomimetic;  
 KW cadherin cell adhesion recognition sequence; CAR; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 XX US2004058864-A1.  
 XX  
 XX 25-MAR-2004.  
 XX  
 XX 10-APR-2003; 2003US-00412701.  
 XX  
 XX 24-JAN-2000; 2000US-00491078.  
 XX  
 XX 24-JAN-2001; 2001US-00769145.  
 XX  
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX  
 XX Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;  
 PI Hu Z;  
 XX  
 XX WPI; 2004-268836/25.  
 XX  
 XX New cell adhesion modulating agent, useful for treating or preventing  
 PT cancer and/or inhibiting metastasis, inhibiting angiogenesis, enhancing  
 PT wound healing, treating a demyelinating neurological disease or treating  
 PT spinal cord injuries.  
 XX  
 XX Disclosure; SEQ ID NO 87; 281pp; English.  
 PS  
 XX The invention relates to a cell adhesion-modulating agent. The invention  
 CC also relates to methods for screening a candidate compound for the  
 CC ability to modulate classical cadherin-mediated cell adhesion,  
 CC identifying a compound that modulates classical cadherin-mediated cell

CC adhesion, modulating classical cadherin-mediated intercellular adhesion,  
 CC reducing unwanted cellular adhesion in a mammal, enhancing the delivery  
 CC of a drug to a tumour in a mammal, inhibiting the development of a cancer  
 CC in a mammal, inhibiting angiogenesis in a mammal, enhancing drug delivery  
 CC to the central nervous system of a mammal, enhancing wound healing in a  
 CC mammal, enhancing adhesion of foreign tissue implanted within a mammal,  
 CC modulating the immune system of a mammal, increasing vasopermeability in  
 CC a mammal, treating a demyelinating neurological disease in a mammal,  
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,  
 CC inhibiting synaptic stability in a mammal, modulating neurite outgrowth,  
 CC treating spinal cord injuries in a mammal and treating macular  
 CC degeneration in a mammal. The compounds are useful for inhibiting or  
 CC enhancing cadherin-mediated cell adhesion. The cell adhesion modulating  
 CC agents are useful for inhibiting the development of cancer, e.g. treating  
 CC or preventing cancer and/or inhibiting metastasis. The cancer is a  
 CC bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The  
 CC agents are also useful in inhibiting angiogenesis, for enhancing the  
 CC delivery of a drug to a tumour in a mammal, for enhancing wound healing in  
 CC a mammal, for enhancing adhesion of foreign tissue implanted within a  
 CC mammal, for modulating the immune system of a mammal, for treating a  
 CC demyelinating neurological disease (such as multiple sclerosis) in a  
 CC mammal, for inhibiting synaptic stability in a mammal, for modulating  
 CC neurite outgrowth, for treating spinal cord injuries in a mammal, for  
 CC treating macular degeneration in a mammal. This sequence represents a  
 CC cadherin-mediated cell adhesion-modulating peptidomimetic, comprising a  
 CC classical cadherin cell adhesion recognition (CAR) sequence.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 100.0%; Score 34; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CHAVC 5  
 DB 2 CHAVC 6  
 |||||  
 RESULT 47  
 AAM47562  
 ID AAM47562 standard; peptide; 8 AA.  
 XX  
 AC AAM47562;  
 XX  
 XX 12-FEB-2002 (first entry)  
 XX  
 DE Cyclic peptide endothelial cell adhesion modulator #22.  
 XX  
 KW Cadherin; cytostatic; gynecological; endometriosis;  
 KW endothelial cell adhesion; angiogenesis; vasopermeability; tumour;  
 KW cyclic.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "Linked to residue 8 to form a cyclic peptide, N-  
 FT terminal acetyl or N-terminal CH3-SO2 group"  
 FT Modified-site 8  
 FT /note= "Linked to residue 1 to form a cyclic peptide, C-  
 FT terminal amide"  
 FT  
 XX WO200177146-A2.  
 XX  
 XX 18-OCT-2001.  
 PD  
 XX 09-APR-2001; 2001WO-US011669.  
 PF  
 XX 07-APR-2000; 2000US-00544782.  
 PR  
 XX (UYMC-) UNIV MCGILL.  
 PA  
 XX

PI Blaschuk OW, Gour BJ, Farookhi R, Ali A;  
 DR WPI; 2002-049129/06.  
 XX  
 PT Modulating endothelial cell adhesion for inhibiting development of  
 PT endometriosis, increasing blood flow to tumor in a mammal, by contacting  
 PT cell with a cyclic peptide having cadherin cell adhesion recognition  
 PT sequence.  
 XX  
 XX Claim 6; Page 64; 139pp; English.  
 PS  
 XX The present invention relates to a method for modulating endothelial cell  
 CC adhesion. The method comprises contacting an endothelial cell with a  
 CC modulating peptide comprising a cadherin cell adhesion recognition  
 CC sequence (His Ala Val) within a cyclic peptide ring. The method is useful  
 CC for inhibiting angiogenesis, increasing vasopermeability, increasing  
 CC blood flow to a tumour, disrupting neovasculature and inhibiting the  
 CC development of endometriosis in a mammal. The modulating peptide reduces  
 CC unwanted endothelial adhesion occurring between tumour cells, tumour  
 CC cells and normal cells, normal cells as a result of surgery, injury,  
 CC chemotherapy, disease and inflammation. The present sequence is one such  
 CC modulating peptide  
 XX  
 SQ Sequence 8 AA;  
  
 Query Match 100.0%; Score 34; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 CHAVC 5  
 DB 3 CHAVC 7  
  
 RESULT 48  
 AAY68110  
 ID AAY68110 standard; protein; 61 AA.  
 XX  
 AC AAY68110;  
 XX  
 DT 13-APR-2000 (first entry)  
 XX  
 DE Kunitz protease inhibitor variant TW6151.  
 XX  
 KW Kunitz protease inhibitor; KPI; serine protease; kallikrein; plasmin;  
 KW amyloid precursor protein; coagulation factor; blood loss; cardiant;  
 KW cardiopulmonary bypass surgery; anticoagulant; anti-inflammatory;  
 KW anti-arthritis; thrombolytic; antirheumatic; antipsoriatic;  
 KW immunosuppressant; pancreatitis; deep vein thrombosis; psoriasis;  
 KW rheumatoid arthritis; myocardial infarction; transplant rejection.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO9963090-A2.  
 XX  
 PD 03-DEC-1999.  
 XX  
 PF 03-JUN-1999; 99WO-US012276.  
 XX  
 PR 03-JUN-1998; 98US-0087885P.  
 XX  
 PA (SCIO-) SCIOS INC.  
 XX  
 PI White RT, Damm D, Lesikar DD, Mcfadden K, Garrick BL, Lucas AB;  
 PI Pollitt NS, Lam AO;  
 XX  
 DR WPI; 2000-105699/09.  
 XX  
 PT Novel enzyme inhibitors especially used to reduce postoperative bleeding.  
 XX  
 PS Example 4; Fig 64; 151pp; English.  
 XX  
 CC The present invention describes protease inhibitors that are analogues of  
 CC the Kunitz protease inhibitor (KPI) domain of the amyloid precursor  
 CC protein. The protease inhibitors can be used to treat or prevent  
 CC disorders associated with increased activity of serine proteases,  
 CC specifically blood loss during surgery (particularly cardiopulmonary  
 CC bypass surgery where plasma proteases are activated by contact with  
 CC surfaces in the heart-lung machine), but also other conditions such as  
 CC pancreatitis; deep vein thrombosis; rheumatoid arthritis; psoriasis;  
 CC myocardial infarction; and transplant rejection. They are also for organ  
 CC preservation and to promote wound healing. In vitro the protease  
 CC inhibitors may be used to inhibit serine proteases during preparation of  
 CC cell extracts. The protease inhibitors are based on a human peptide  
 CC sequence so are unlikely to be immunogenic, can be produced at high  
 CC levels in recombinant expression systems, and can inhibit a wide range of  
 CC serine proteases. They are more potent or specific than known inhibitors.  
 CC The present sequence represents a KPI variant which is given in an  
 CC example from the present invention  
 XX  
 SQ Sequence 61 AA;  
  
 Query Match 100.0%; Score 34; DB 3; Length 61;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 CHAVC 5  
 DB 53 CHAVC 57  
  
 RESULT 49  
 AAY68085  
 ID AAY68085 standard; protein; 61 AA.  
 XX  
 AC AAY68085;  
 XX  
 DT 13-APR-2000 (first entry)  
 XX  
 DE Kunitz protease inhibitor variant TW6182.  
 XX  
 KW Kunitz protease inhibitor; KPI; serine protease; kallikrein; plasmin;  
 KW amyloid precursor protein; coagulation factor; blood loss; cardiant;  
 KW cardiopulmonary bypass surgery; anticoagulant; anti-inflammatory;  
 KW anti-arthritis; thrombolytic; antirheumatic; antipsoriatic;  
 KW immunosuppressant; pancreatitis; deep vein thrombosis; psoriasis;  
 KW rheumatoid arthritis; myocardial infarction; transplant rejection.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO9963090-A2.  
 XX  
 PD 09-DEC-1999.  
 XX  
 PF 03-JUN-1999; 99WO-US012276.  
 XX  
 PR 03-JUN-1998; 98US-0087885P.  
 XX  
 PA (SCIO-) SCIOS INC.  
 XX  
 PI White RT, Damm D, Lesikar DD, Mcfadden K, Garrick BL, Lucas AB;  
 PI Pollitt NS, Lam AO;  
 XX  
 DR WPI; 2000-105699/09.  
 XX  
 PT Novel enzyme inhibitors especially used to reduce postoperative bleeding.  
 XX  
 PS Example 4; Fig 64; 151pp; English.  
 XX  
 CC The present invention describes protease inhibitors that are analogues of  
 CC the Kunitz protease inhibitor (KPI) domain of the amyloid precursor  
 CC protein. The protease inhibitors can be used to treat or prevent  
 CC disorders associated with increased activity of serine proteases,  
 CC specifically blood loss during surgery (particularly cardiopulmonary

CC bypass surgery where plasma proteases are activated by contact with  
 CC surfaces in the heart-lung machine), but also other conditions such as  
 CC pancreatitis; deep vein thrombosis; rheumatoid arthritis; pericarditis;  
 CC myocardial infarction; and transplant rejection. They are also for organ  
 CC preservation and to promote wound healing. In vitro the protease  
 CC inhibitors may be used to inhibit serine proteases during preparation of  
 CC cell extracts. The protease inhibitors are based on a human peptide  
 CC sequence so are unlikely to be immunogenic, can be produced at high  
 CC levels in recombinant expression systems, and can inhibit a wide range of  
 CC serine proteases. They are more potent or specific than known inhibitors.  
 CC The present sequence represents a KPI variant which is given in an  
 CC example from the present invention  
 XX

SQ Sequence 61 AA;

Query Match 100.0%; Score 34; DB 3; Length 61;

Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0;

Qy 1 CHAVC 5

Db 53 CHAVC 57  
 |||||

RESULT 50

ID AAU28273 standard; protein; 121 AA.

AC AAU28273;

DT 18-DEC-2001 (first entry)

DE Novel human secretory protein, Seq ID No 630.

KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;  
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;  
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;  
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;  
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;  
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;  
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;  
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;  
 KW fertility; analgesic; pain; antigen.

OS Homo sapiens.

PN WO200166689-A2.

PD 13-SEP-2001.

PF 05-MAR-2001; 2001WO-US004942.

PR 07-MAR-2000; 2000US-00519705.

PR 19-MAY-2000; 2000US-00574454.

PR 17-JUN-2000; 2000US-00596193.

PR 14-JUL-2000; 2000US-00616847.

PR 19-SEP-2000; 2000US-00665363.

PR 20-OCT-2000; 2000US-00693267.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;

PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;

XX WPI; 2001-589934/66.

DR N-PSDB; AAS45173.

XX Novel polypeptides and nucleic acids obtained from cDNA libraries

PT prepared from various human tissues, for diagnosis and treatment of

PT cancer, neurological, inflammatory, and autoimmune disorders.

XX Example 2; SEQ ID NO 630; 107pp; English.

PS

XX

CC The invention relates to novel isolated human secreted polypeptides (I)  
 CC and polynucleotides (II). (I) and (II) are useful for treating  
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,  
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is  
 CC involved in increasing haematopoiesis, stem cell survival, bone growth  
 CC and remodeling. (I), (II) and modulators of (II) are useful for  
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for  
 CC creating transgenic animals useful for studying the in vivo activities of  
 CC the polypeptide as well as for studying modulators of the polypeptides.  
 CC (I) induces the proliferation of neural cells and regeneration of nerve  
 CC and brain tissue and is useful for the treatment of central and  
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,  
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral  
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic  
 CC activity, regulation of haematopoiesis and is useful for treating myeloid  
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia  
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve  
 CC tissue growth, and in tissue repair, healing of burns, incisions, ulcers,  
 CC for treating osteoporosis, osteoarthritis, bone degenerative disorders,  
 CC or periodontal disease. Furthermore, (I) is also useful for gut  
 CC protection or regeneration and treatment of lung or liver fibrosis,  
 CC reperfusion injury in various tissues, various immune deficiencies and  
 CC disorders including severe combined immunodeficiency (SCID), bacterial or  
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,  
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic  
 CC reactions and conditions, such as asthma or other respiratory problems.  
 CC In addition, (I) affects biohythms or circadian cycles of rhythms,  
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of  
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides  
 CC analgesic effects or other pain reducing effects, immunoglobulin like  
 CC activity and can act as an antigen in a vaccine composition to raise an  
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein  
 CC amino acid sequences of the invention  
 XX

SQ Sequence 121 AA;

Query Match 100.0%; Score 34; DB 4; Length 121;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 61 CHAVC 65  
 |||||

RESULT 51

AAG38298

ID AAG38298 standard; protein; 198 AA.

AC AAG38298;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 47228.

XX Protein identification; signal transduction pathway; metabolic pathway;  
 XX hybridisation assay; genetic mapping; gene expression control; promoter;  
 XX termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

PR 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135829P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 28-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.

PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 20-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
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PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
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Query Match 100.0%; Score 34; DB 3; Length 198;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 60 CHAVC 64

RESULT 52
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ID AAG07319 standard; protein; 198 AA.
XX
AC AAG07319;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4428.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
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Query Match 100.0%; Score 34; DB 3; Length 198;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
DB 60 CHAVC 64

RESULT 53

AG38297

ID AAG38297 standard; protein; 244 AA.

XX AAG38297;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 47227.

XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.  
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PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
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Query Match 100.0%; Score 34; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 106 CHAVC 110

RESULT 55
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ID ABB67444 standard; protein; 380 AA.
XX AC ABB67444;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 29124.
XX KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX (PEKE ) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX N-PSDB; ABL11547.
XX New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.
XX Disclosure; SEQ ID NO 29124; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABBS72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 380 AA;

Query Match 100.0%; Score 34; DB 4; Length 380;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 106 CHAVC 110
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PA (GENO-) GENOME THERAPEUTICS CORP.  
XX Smith DR, Mao J;  
PI WPI; 2003-656441/62.  
XX New Mycobacterium tuberculosis anion pump peptide useful for as  
XX tuberculosis vaccine and diagnosis of tuberculosis infection.  
PT  
XX Disclosure; SEQ ID NO 213; 26pp; English.  
XX  
CC The invention relates to a non-naturally occurring peptide of  
CC Mycobacterium tuberculosis comprising an amino acid sequence  
CC corresponding to an anion pump protein. The invention also relates to a  
CC non-naturally occurring nucleic acid corresponding to a DNA sequence of  
CC Mycobacterium tuberculosis or Mycobacterium leprae. The new peptide is  
CC useful as a vaccine against Mycobacterium tuberculosis or Mycobacterium  
CC leprae or for screening for new tuberculosis drugs. Purified proteins  
CC derived from the sequences of the invention may elicit a specific immune  
CC response. The peptide may also be used to detect hypersensitivity  
CC reactions of individuals exposed to Mycobacterium tuberculosis or  
CC Mycobacterium leprae. The proteins and peptides may be affixed to solid  
CC supports to detect antibodies typical of hypersensitivity reactions, from  
CC a patient's sera. This sequence represents Mycobacterium leprae non-  
CC naturally occurring peptide of the invention. Note: The sequence data for  
CC this patent did not form part of the printed specification but was  
CC obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html.  
XX  
XX Sequence 542 AA;  
SQ

Query Match 100.0%; Score 34; DB 7; Length 542;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CHAVC 5  
Db 1 CHAVC 5  
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1 CHAVC 5

RESULT 59  
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AC ADK16783;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Nanoarchaeum equitans cancer-associated (CA) protein #367.  
XX  
KW cancer-associated gene; CA gene; cancer; carcinoma; lymphoma; leukaemia.  
XX  
OS Nanoarchaeum equitans.  
XX  
FN WO2003093434-A2.  
XX  
PD 13-NOV-2003.  
XX  
PF 01-MAY-2003; 2003WO-US013699.  
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PR 01-MAY-2002; 2002US-0377447P.  
XX  
PS (DIVE-) DIVERSA CORP.  
XX  
PI Stetter KO, Waters E, Kretz K, Podar M, Richardson T,  
PI Noordewier M;  
XX  
XX WPI; 2004-053041/05.  
DR N-PSDB; ADK16782.  
XX  
XX New recombinant cancer-associated genes, such as KGNJ9, useful for  
PT diagnosing or treating carcinoma, e.g. breast, colon, rectal, pancreatic,  
PT cervical, or skin cancers, lymphomas, or leukemia.  
PT

XX Claim 64; SEQ ID NO 735; 251pp; English.  
XX  
CC The invention comprises then amino acid and coding sequences of cancer-  
CC associated (CA) genes isolated from Nanoarchaeum equitans. The invention  
CC also comprises the Nanoarchaeum equitans genome. The DNA and protein  
CC sequences of the invention are useful for diagnosing and treating cancer  
CC (e.g. carcinoma, lymphoma, or leukaemia). The present amino acid sequence  
CC represents a Nanoarchaeum equitans CA protein of the invention.  
XX  
XX Sequence 75 AA;  
SQ

Query Match 97.1%; Score 33; DB 8; Length 75;  
Best Local Similarity 80.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CHAVC 5  
Db 17 CHAIC 21  
|||||  
17 CHAIC 21

RESULT 60  
AAU50581  
ID AAU50581 standard; protein; 176 AA.  
XX  
AC AAU50581;  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DE Propionibacterium acnes immunogenic protein #11477.  
XX  
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;  
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
KW dermatological; osteopathic; neuroprotectant.  
XX  
OS Propionibacterium acnes.  
XX  
FN WO200181581-A2.  
XX  
PD 01-NOV-2001.  
XX  
PF 20-APR-2001; 2001WO-US012865.  
XX  
PR 21-APR-2000; 2000US-0199047P.  
PR 02-JUN-2000; 2000US-0208841P.  
PR 07-JUL-2000; 2000US-0216747P.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;  
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;  
XX  
DR WPI; 2001-616774/71.  
DR N-PSDB; AAS59549.  
XX  
PT Propionibacterium acnes polypeptides and nucleic acids useful for  
PT vaccinating against and diagnosing infections, especially useful for  
PT treating acne vulgaris.  
XX  
PS Example 1; SEQ ID NO 11776; 1069pp; English.  
XX  
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic  
CC polypeptides. The proteins and their associated DNA sequences are used in  
CC the treatment, prevention and diagnosis of medical conditions caused by  
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,  
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.  
CC P. acnes is also involved in infections of bone, joints and the central  
CC nervous system, however it is particularly involved in the inflammatory  
CC lesions associated with acne vulgaris. A method for detecting the  
CC presence or absence of P. acnes in a patient comprises contacting a  
CC sample with a binding agent that binds to the proteins of the invention  
CC and determining the amount of bound protein in the sample. The

CC polypeptides may be used as antigens in the production of antibodies  
 CC specific for P. acnes proteins. These antibodies can be used to  
 CC downregulate expression and activity of P. acnes polypeptides and  
 CC therefore treat P. acnes infections. The antibodies may also be used as  
 CC diagnostic agents for determining P. acnes presence, for example, by  
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for  
 CC this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 XX Sequence 176 AA;  
 SQ

Query Match 97.1%; Score 33; DB 4; Length 176;  
 Best Local Similarity 80.0%; Pred. No. 6.9e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
 Db 53 CHAIC 57  
 |||:|

RESULT 61  
 ABM47100  
 ID ABM47100 standard; protein; 176 AA.  
 XX  
 AC ABM47100;  
 XX  
 XX  
 DT 20-OCT-2003 (first entry)  
 XX  
 DE Propionibacterium acnes predicted ORF-encoded polypeptide #11776.  
 XX  
 XX  
 XX Acne vulgaris; antiseborrheic; dermatological; antibacterial;  
 KW immunostimulant; immune response; vaccine.  
 XX  
 OS Propionibacterium acnes.  
 XX  
 XX  
 PN W02003033515-A1.  
 XX  
 PD 24-APR-2003.  
 XX  
 XX 11-OCT-2002; 2002WO-US032727.  
 XX  
 XX 15-OCT-2001; 2001US-00978825.  
 PR  
 XX (CORI-) CORIXA CORP.  
 PA  
 XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;  
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;  
 PI Barth B, Vallieue-Douglass J;  
 XX  
 XX WPI; 2003-381789/36.  
 DR N-PSDB; ACF64478.  
 DR  
 XX

New Propionibacterium acnes polypeptides and polynucleotides encoding the  
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,  
 PT or for stimulating an immune response specific for a P. acnes protein.  
 XX  
 PS Example 1; SEQ ID NO 11776; 1481pp; English.

The invention relates to an isolated polynucleotide (ACF64435-ACF64733)  
 CC encoding a Propionibacterium acnes protein. The invention also relates to  
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to  
 CC immunogenic fragments of P. acnes polypeptides. The invention  
 CC additionally encompasses expression vectors and host cells comprising a  
 CC polynucleotide of the invention; antibodies against polypeptides of the  
 CC polynucleotide; fusion proteins comprising a polypeptide of the invention; a  
 CC method for stimulating an immune response specific for a P. acnes  
 CC polypeptide and an isolated T cell population comprising T cells prepared  
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,  
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or  
 CC antigen-presenting cells that express the polypeptide); a method and kit  
 CC for detecting or determining the presence or absence of P. acnes in a  
 CC patient; and a method for inhibiting the development of P. acnes in a

CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion  
 CC proteins, T cell populations or antigen-presenting cells that express the  
 CC polypeptides are useful for diagnosing, preventing or treating acne  
 CC vulgaris, or for stimulating an immune response specific for a P. acnes  
 CC protein. The polynucleotides can also be used as probes or primers for  
 CC nucleic acid hybridisation. The vaccine composition is useful for the  
 CC stimulation of an immune response against P. acnes, or for treating acne,  
 CC and the kit is useful for performing a diagnostic assay. The present  
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open  
 CC reading frame) contained within the P. acnes polynucleotides of the  
 CC invention. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 XX Sequence 176 AA;  
 SQ

Query Match 97.1%; Score 33; DB 6; Length 176;  
 Best Local Similarity 80.0%; Pred. No. 6.9e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
 Db 53 CHAIC 57  
 |||:|

RESULT 62  
 ABB92762  
 ID ABB92762 standard; protein; 428 AA.  
 XX  
 AC ABB92762;  
 XX  
 DT 31-MAY-2002 (first entry)  
 XX  
 DE Herbicidally active polypeptide SEQ ID NO 1973.  
 XX  
 KW Herbicidal; plant; agriculture; herbicide.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN W0200210210-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 XX 28-AUG-2001; 2001WO-EP009892.  
 PF  
 XX 28-AUG-2001; 2001WO-EP009892.  
 PR (FARB ) BAYER AG.  
 XX  
 XX Tietjen K, Weidler M;  
 PI  
 XX WPI; 2002-269010/31.  
 DR

Identifying plant target proteins for herbicidally active compounds,  
 PT comprising aligning and comparing nucleic acid or amino acid sequences  
 PT from plant with nucleic acid or amino acid sequences from non-plant  
 PT organisms.  
 XX  
 XX Claim 5; SEQ ID NO 1973; 261pp + Sequence Listing; English.

The invention relates to identifying target proteins (ABB90790-ABB94016)  
 CC for herbicidally active compounds, comprising aligning and comparing  
 CC nucleic acid or amino acid sequences from plant with nucleic acid or  
 CC amino acid sequences from non-plant organisms using suitable search  
 CC parameters, where plant sequences having an E-value greater by a factor  
 CC of 3 than the E-value of most similar non-plant sequences are selected.  
 CC The polypeptides or nucleic acids encoding them are useful for  
 CC identifying modulators. The identified modulators are useful as  
 CC herbicides  
 XX  
 SQ Sequence 428 AA;  
 Query Match 97.1%; Score 33; DB 5; Length 428;





XX Key Location/Qualifiers  
 FH Misc-difference 363 /note= "Wild type Thr substituted with Ala"  
 FT  
 PT  
 PN  
 PN  
 XX EP1077260-A1.  
 XX  
 PD 21-FEB-2001.  
 XX  
 PF 13-AUG-1999; 99EP-00115161.  
 XX  
 PR 13-AUG-1999; 99EP-00115161.  
 XX  
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX  
 PI Nueesch J, Rommelaere J;  
 XX  
 XX WPI; 2001-212717/22.  
 DR N-PSDB; AAD02801.  
 XX  
 PT Novel parvovirus non-structure protein variant, useful for treating  
 PT tumoral diseases, has a shifted equilibrium between DNA replication and  
 PT transcription activities, and cytotoxic activity.  
 PS  
 PS Claim 6; Page 19-21; 41pp; English.  
 XX  
 CC The present sequence is parvovirus non-structure protein 1 (NS1) variant  
 CC (T363A). The invention relates to the variants of the parvovirus non-  
 CC structure protein (NS1) having a shifted equilibrium between the DNA  
 CC replication and transcription activities, and the cytotoxicity activity.  
 CC These variants are useful as toxins for treating tumoural diseases. The  
 CC variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-  
 CC 2003 to correct OS field.)  
 XX  
 SQ Sequence 672 AA;  
 Query Match 97.1%; Score 33; DB 4; Length 672;  
 Best Local Similarity 80.0%; Pred. No. 2.1e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CHAVC 5  
 Db 378 CHAIC 382  
 XX  
 RESULT 66  
 AAY72702  
 ID AAY72702 standard; protein; 672 AA.  
 XX  
 AC AAY72702;  
 XX  
 DT 06-AUG-2003 (revised)  
 DT 31-MAY-2001 (first entry)  
 XX  
 DE Parvovirus wild-type non-structure protein 1 (NS1).  
 XX  
 KW NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy;  
 KW tumoural disease; gene therapy.  
 XX  
 OS Parvovirus.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 283 /note= "Wild type Ser substituted with Ala"  
 XX  
 PN EP1077260-A1.  
 XX  
 PD 21-FEB-2001.  
 XX  
 PF 13-AUG-1999; 99EP-00115161.  
 XX  
 PR 13-AUG-1999; 99EP-00115161.  
 XX  
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX  
 PI Nueesch J, Rommelaere J;  
 XX  
 XX WPI; 2001-212717/22.  
 DR N-PSDB; AAD02799.  
 XX  
 PT Novel parvovirus non-structure protein variant, useful for treating  
 PT tumoral diseases, has a shifted equilibrium between DNA replication and  
 PT transcription activities, and cytotoxic activity.  
 PS  
 PS Claim 6; Page 14-16; 41pp; English.  
 XX  
 CC The present sequence is parvovirus non-structure protein 1 (NS1) variant  
 CC (S283A). The invention relates to the variants of the parvovirus non-  
 CC structure protein (NS1) having a shifted equilibrium between the DNA

DR WPI; 2001-212717/22.  
 DR N-PSDB; AAD02797.  
 XX  
 PT Novel parvovirus non-structure protein variant, useful for treating  
 PT tumoral diseases, has a shifted equilibrium between DNA replication and  
 PT transcription activities, and cytotoxic activity.  
 XX  
 PS Disclosure; Fig 1; 41pp; English.  
 XX  
 CC The present sequence is a parvovirus wild-type non-structure protein 1  
 CC (NS1). The present invention relates to the variants of the parvovirus  
 CC non-structure protein (NS1) having a shifted equilibrium between the DNA  
 CC replication and transcription activities, and the cytotoxicity activity.  
 CC These variants are useful as toxins for treating tumoural diseases. The  
 CC variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-  
 CC 2003 to correct OS field.)  
 XX  
 SQ Sequence 672 AA;  
 Query Match 97.1%; Score 33; DB 4; Length 672;  
 Best Local Similarity 80.0%; Pred. No. 2.1e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CHAVC 5  
 Db 378 CHAIC 382  
 XX  
 RESULT 67  
 AAY72704  
 ID AAY72704 standard; protein; 672 AA.  
 XX  
 AC AAY72704;  
 XX  
 DT 06-AUG-2003 (revised)  
 DT 31-MAY-2001 (first entry)  
 XX  
 DE Parvovirus non-structure protein 1 (NS1) variant (S283A).  
 XX  
 KW NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy;  
 KW tumoural disease; gene therapy; mutant; mutein; variant.  
 XX  
 OS Parvovirus.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 283 /note= "Wild type Ser substituted with Ala"  
 XX  
 PN EP1077260-A1.  
 XX  
 PD 21-FEB-2001.  
 XX  
 PF 13-AUG-1999; 99EP-00115161.  
 XX  
 PR 13-AUG-1999; 99EP-00115161.  
 XX  
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX  
 PI Nueesch J, Rommelaere J;  
 XX  
 XX WPI; 2001-212717/22.  
 DR N-PSDB; AAD02799.  
 XX  
 PT Novel parvovirus non-structure protein variant, useful for treating  
 PT tumoral diseases, has a shifted equilibrium between DNA replication and  
 PT transcription activities, and cytotoxic activity.  
 XX  
 PS Claim 6; Page 14-16; 41pp; English.  
 XX  
 CC The present sequence is parvovirus non-structure protein 1 (NS1) variant  
 CC (S283A). The invention relates to the variants of the parvovirus non-  
 CC structure protein (NS1) having a shifted equilibrium between the DNA

CC replication and transcription activities, and the cytotoxicity activity.  
 CC These variants are useful as toxins for treating tumoural diseases. The  
 CC variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-  
 CC 2003 to correct OS field.)  
 XX  
 SQ Sequence 672 AA;

Query Match 97.1%; Score 33; DB 4; Length 672;  
 Best Local Similarity 80.0%; Pred. No. 2.1e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 Db 378 CHAIC 382  
 |||:|

# RESULT 68

ADO34065  
 ID ADO34065 standard; peptide; 16 AA.

XX  
 AC ADO34065;

DT 26-AUG-2004 (first entry)

XX Human CLA2.3 peptide fragment, SEQ ID 28.

DE Cytostatic; human; Colorectal Lesion Associated 2; CLA2; chromosome 5p14;  
 KW proliferative disorder; tumour; cancer; carcinoma; dysplasia.  
 XX Homo sapiens.

OS  
 XX  
 PN EPI426442-A1.

XX  
 PD 09-JUN-2004.

XX 02-DEC-2002; 2002EP-00026772.

XX 02-DEC-2002; 2002EP-00026772.

XX (MTM-) MTM LAB AG.

PA Hipfel R;

XX WPI; 2004-422595/40.

XX New isolated colorectal lesion associated nucleic acid molecule useful in  
 PT the detection and therapy of proliferative disorders.  
 XX Claim 6; SEQ ID NO 28; 123pp; English.

XX The present invention relates to the human Colorectal Lesion Associated 2  
 CC (CLA2) gene (I; ADO34039), which is located on chromosome 5p14. CLA2  
 CC sequences are useful for the detection and treatment of proliferative  
 CC disorders such as: a benign and malignant tumour (head, neck, respiratory  
 CC tract, gastrointestinal tract, skin and its appendages, central and  
 CC peripheral nervous system, urinary system, reproductive system, endocrine  
 CC system, soft tissues and bone, lymphopoietic and haematopoietic system,  
 CC breast, anogenital or colorectal cancers), a carcinoma or a dysplasia.  
 CC The present sequence was used to illustrate the invention.  
 XX  
 SQ Sequence 16 AA;

Query Match 91.2%; Score 31; DB 8; Length 16;  
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 Db 1 CHALC 5  
 |||:|

# RESULT 69

AAM15812

ID AAM15812 standard; protein; 20 AA.

XX  
 AC AAM15812;

XX 12-OCT-2001 (first entry)

XX Peptide #2246 encoded by probe for measuring cervical gene expression.

DE Probe; human; microarray; gene expression; cervical epithelial cell;  
 KW cervical cancer.

XX Homo sapiens.

OS  
 PN WO200157278-A2.

XX 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US0000670.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488901/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human cervical epithelial cells.

XX Claim 27; SEQ ID NO 20638; 487pp; English.

XX The present invention relates to human single exon nucleic acid probes  
 CC (SENP; see AAI10068-AAI28459). The present sequence is a peptide encoded  
 CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs  
 CC can be used to produce a single exon microarray, which can be used for  
 CC measuring human gene expression in a sample derived from human cervical  
 CC epithelial cells. By measuring gene expression, the probes are therefore  
 CC useful in grading and/or staging of diseases of the cervix, notably  
 CC cervical cancer. Note: The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 20 AA;

Query Match 91.2%; Score 31; DB 4; Length 20;  
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 |||:|

Db 1 CHALC 5  
 |||:|

# RESULT 70

ABB34809

ID ABB34809 standard; peptide; 20 AA.

XX  
 AC ABB34809;

XX 04-FEB-2002 (first entry)

XX Peptide #2315 encoded by human foetal liver single exon probe.

DE Human; foetal liver; gene expression; single exon nucleic acid probe.

XX Homo sapiens.

OS

XX WO200157277-A2.  
PN  
XX  
XX 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US000669.  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-483447/52.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.  
PT  
XX  
XX Claim 27; SEQ ID NO 27444; 639pp + Sequence Listing; English.  
XX  
XX The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 20 AA;  
SQ  
Query Match 91.2%; Score 31; DB 4; Length 20;  
Best Local Similarity 80.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CHAVC 5  
Db |||:|  
1 CHALC 5  
RESULT 71  
AAM28322  
ID AAM28322 standard; protein; 20 AA.  
XX  
XX AAM28322;  
AC  
XX 17-OCT-2001 (first entry)  
DT  
XX Peptide #2359 encoded by probe for measuring placental gene expression.  
DE  
XX Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.  
KW  
KW Homo sapiens.  
XX  
XX WO200157272-A2.  
PN  
XX 09-AUG-2001.  
PD  
XX 30-JAN-2001; 2001WO-US000663.  
PF  
XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR

PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488897/53.  
DR  
XX Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.  
PT  
XX  
XX Claim 27; SEQ ID NO 28591; 654pp; English.  
PS  
XX The present invention relates to single exon nucleic acid probes (SENP: see AA1315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders  
CC  
XX Sequence 20 AA;  
SQ  
Query Match 91.2%; Score 31; DB 4; Length 20;  
Best Local Similarity 80.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CHAVC 5  
Db |||:|  
1 CHALC 5  
RESULT 72  
ABB29631  
ID ABB29631 standard; peptide; 20 AA.  
XX  
XX ABB29631;  
AC  
XX 01-FEB-2002 (first entry)  
DT  
XX Peptide #2282 encoded by breast cell single exon nucleic acid probe.  
DE  
XX Human; microarray; single exon probe; gene expression; breast; disease; cancer.  
KW  
KW Homo sapiens.  
XX  
XX WO200157271-A2.  
PN  
XX 09-AUG-2001.  
PD  
XX 30-JAN-2001; 2001WO-US000662.  
PF  
XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-496933/54.  
DR  
XX New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.  
PT  
XX  
XX Claim 27; SEQ ID NO 12599; 327pp + Sequence Listing; English.  
PS  
XX The invention relates to a spatially-addressable set of single exon  
CC

CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human breast and Br 474 cells. The method involves contacting the  
 CC probes with a collection of detectably labelled nucleic acids derived  
 CC from mRNA of human breast, and then measuring the label bound to each  
 CC probe of the microarray. The probes are useful for verifying the  
 CC expression of regions of genomic DNA predicted to encode proteins. They  
 CC are useful for gene discovery, and for determining predisposition and/or  
 CC prognosing breast disease. Gene expression analysis is useful for  
 CC assessing the toxicity of chemical agents on cells. The microarray of  
 CC this invention presents a far greater diversity of probes for measuring  
 CC gene expression, with far less bias than expressed sequence tag  
 CC microarrays. The method is suitable for rapid production of functional  
 CC information from genomic sequence. The present sequence is a peptide  
 CC encoded by a single exon nucleic acid probe of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 AA;

Query Match 91.2%; Score 31; DB 4; Length 20;  
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 Db 1 CHALC 5  
 |||:|

## RESULT 73

ABB20225  
 ID ABB20225 standard; protein; 20 AA.

XX  
 AC ABB20225;

DT 23-JAN-2002 (first entry)

DE Protein #2224 encoded by probe for measuring heart cell gene expression.

XX Human; gene expression; heart; microarray; vascular system;  
 KW cardiovascular disease; hypertension; cardiac arrhythmia;  
 KW congenital heart disease.

XX Homo sapiens.

XX WO200157274-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000666.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488990/53.

XX Single exon nucleic acid probes for analyzing gene expression in human  
 XX hearts.  
 XX Claim 15; SEQ ID NO 21995; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for  
 CC measuring human gene expression in a sample derived from human heart (see  
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such

CC probe. The probes may be used for predicting, measuring and displaying  
 CC gene expression in samples derived from the human heart via microarrays.  
 CC By measuring gene expression, the probes are useful for predicting,  
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the  
 CC human heart and vascular system e.g. cardiovascular disease,  
 CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX

SQ Sequence 20 AA;

Query Match 91.2%; Score 31; DB 4; Length 20;  
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 Db 1 CHALC 5  
 |||:|

## RESULT 74

AAM67996  
 ID AAM67996 standard; protein; 20 AA.

XX  
 AC AAM67996;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28302.

XX Human; bone marrow expressed exon; gene expression analysis; probe;  
 KW microarray; cancer; leukaemia; lymphoma; myeloma.

XX Homo sapiens.

XX WO200157276-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000668.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488990/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing  
 XX gene expression in human bone marrow.  
 XX Example 4; SEQ ID NO 28302; 658pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC bone marrow. They can be used to measure gene expression in bone marrow  
 CC samples, which may enable the improved diagnosis and treatment of cancers  
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a  
 CC protein encoded by one of the probes of the invention

XX Sequence 20 AA;

Query Match 91.2%; Score 31; DB 4; Length 20;  
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

OY      1 CHAVC 5
Db      |||:|
        1 CHALC 5

RESULT 75
AAM55611
ID AAM55611 standard; protein; 20 AA.
XX
AC AAM55611;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 27716.
XX
DE Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
OS Homo sapiens.
XX
FN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX Example 4; SEQ ID NO 27716; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention
XX
SQ Sequence 20 AA;
Query Match          91.2%; Score 31; DB 4; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 CHAVC 5
Db      |||:|
        1 CHALC 5

RESULT 76
ABG49637
ID ABG49637 standard; peptide; 20 AA.
XX
AC ABG49637;
XX
DT 25-FEB-2003 (first entry)
XX
XX

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DE      Human liver peptide, SEQ ID NO 28285.
XX
KW      Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW      hypercholesterolaemia; coronary heart disease.
XX
OS      Homo sapiens.
XX
PN      WO200157273-A2.
XX
PD      09-AUG-2001.
XX
PF      30-JAN-2001; 2001WO-US000664.
XX
PR      04-FEB-2000; 2000US-0180312P.
PR      26-MAY-2000; 2000US-0207456P.
PR      30-JUN-2000; 2000US-00608408.
PR      03-AUG-2000; 2000US-00632366.
PR      21-SEP-2000; 2000US-0234687P.
PR      27-SEP-2000; 2000US-0236359P.
PR      04-OCT-2000; 2000GB-00024263.
XX
XX      (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX      Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX      WPI; 2001-488898/53.
XX
XX      Human genome-derived single exon nucleic acid probes useful for analyzing
XX      gene expression in human adult liver.
XX
XX      Claim 27; SEQ ID NO 28285; 650pp; English.
XX
CC      The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC      measuring human gene expression in a sample derived from human adult
CC      liver, comprising one of 13109 defined nucleotide sequences given in the
CC      specification (or complements/ fragments). The probe hybridises at high
CC      stringency to a nucleic acid molecule expressed in the human adult liver.
CC      (I) may be used for predicting, measuring and displaying gene expression
CC      in samples derived from human adult liver. The genes identified may be
CC      involved in genetic liver diseases such as cirrhosis,
CC      hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC      associated with coronary heart disease. ABG47348-ABG59930 represent human
CC      liver single exon encoded peptides of the invention. Note: The sequence
CC      information for this patent does not appear in the printed specification
CC      but was obtained in electronic format directly from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 20 AA;
Query Match          91.2%; Score 31; DB 4; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 CHAVC 5
Db      |||:|
        1 CHALC 5

RESULT 77
AAM03550
ID AAM03550 standard; protein; 20 AA.
XX
AC AAM03550;
XX
XX      09-OCT-2001 (first entry)
XX
DE      Peptide #2232 encoded by probe for measuring breast gene expression.
XX
KW      Probe; human; breast disease; breast cancer; development disorder;
KW      inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
XX      Homo sapiens.
XX
XX

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PN WO200157270-A2.
XX 09-AUG-2001.
XX 29-JAN-2001; 2001WO-US000661.
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-476286/51.
XX Novel single exon nucleic acid probe used to measuring gene expression in
XX a human breast.
XX Claim 27; SEQ ID NO 12290; 322pp; English.
XX The present invention relates to novel single exon nucleic acid probes
XX (see AAI00010-AAI10067). The present sequence is a peptide encoded by one
XX such probe. The probes are useful for measuring human gene expression in
XX a human breast sample, where the probe hybridizes at high stringency to a
XX nucleic acid expressed in the human breast. The probes are useful for
XX predicting, diagnosing, grading, staging, monitoring and prognosing
XX diseases of the human breast, particularly those diseases with polygenic
XX aetiology. The diseases include: breast cancer, disorders of development,
XX inflammatory diseases of the breast, fibrocystic changes, proliferative,
XX breast disease and non-carcinoma tumours. Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 20 AA;
XX Query Match 91.2%; Score 31; DB 4; Length 20;
XX Best Local Similarity 80.0%; Pred. No. 2.3e+02;
XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX Qy 1 CHAUC 5
XX Db 1 CHALC 5
XX RESULT 78
XX ABG37528
XX ID ABG37528 standard; peptide; 20 AA.
XX AC ABG37528;
XX AC ABG37528;
XX 19-AUG-2002 (first entry)
XX Human peptide encoded by genome-derived single exon probe SEQ ID 27193.
XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
XX chronic obstructive pulmonary disease; interstitial lung disease;
XX familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
XX pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX primary ciliary dyskinesia; pulmonary hypertension;
XX hyaline membrane disease.
XX Homo sapiens.
XX OS
XX WO200186003-A2.
XX PN

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XX 15-NOV-2001.
XX 30-JAN-2001; 2001WO-US000665.
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2002-114183/15.
XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples.
XX Claim 27; SEQ ID NO 27193; 634pp; English.
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 13614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of probes
XX; the novel set of probes which hybridise at high stringency to a nucleic
XX acid expressed in the human lung; measuring gene expression in a sample
XX derived from human lung, comprising (a) contacting the array with a
XX collection of detectably labeled nucleic acids derived from human lung
XX mRNA, and (b) measuring the label detectably bound to each probe of the
XX array; identifying exons in a eukaryotic genome, comprising (a)
XX algorithmically predicting at least one exon from genomic sequences of
XX the eukaryote; and (b) detecting specific hybridisation of detectably
XX labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
XX having a fragment identical to the predicted exon, the probe is included
XX in the above mentioned microarray; assigning exons to a single gene,
XX comprising (a) identifying exons from genomic sequence by the method
XX above and (b) measuring the expression of each of the exons in several
XX tissues and/or cell types using hybridisation to a single exon
XX microarrays having a probe with the exon, where a common pattern of
XX expression of the exons in the tissues and/or cell types indicates that
XX the exons should be assigned to a single gene; a peptide comprising one
XX of 12011 sequences, mentioned in the specification, or encoded by the
XX probes/open reading frames (ORF). The probes are used for gene expression
XX analysis, and for identifying exons in a gene, particularly using human
XX lung derived mRNA and for the study of lung diseases such as asthma, lung
XX cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
XX disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
XX tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
XX Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
XX histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
XX Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
XX dyskinesia, pulmonary hypertension and hyaline membrane disease. The
XX present sequence is a peptide/protein encoded by a single exon probe of
XX the invention. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 20 AA;
XX Query Match 91.2%; Score 31; DB 5; Length 20;
XX Best Local Similarity 80.0%; Pred. No. 2.3e+02;
XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX Qy 1 CHAUC 5
XX Db 1 CHALC 5

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Qy 1 CHAVC 5  
 ||:|  
 Db 44 CHSVC 48

RESULT 81  
 AA009658  
 ID AAO09658 standard; protein; 61 AA.  
 XX  
 AC AAO09658;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human polypeptide SEQ ID NO 23550.  
 XX  
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorders; arthritis; inflammation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200164835-A2.  
 XX  
 PD 07-SEP-2001.  
 XX  
 PP 26-FEB-2001; 2001WO-US004927.  
 XX  
 PR 28-FEB-2000; 2000US-00515126.  
 PR 18-MAY-2000; 2000US-00577409.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Drmanac RT;  
 XX  
 DR WPI; 2001-514838/56.  
 DR N-PSDB; AAI89589.  
 XX  
 PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing  
 PT and treating e.g. leukemia, inflammation and immune disorders.  
 XX  
 PS Claim 20; SEQ ID NO 23550; 1399pp + Sequence Listing; English.  
 XX  
 CC The invention relates to human polynucleotides (AAI79941-AAI93841) and  
 CC the encoded proteins (AAO0010-AAO13910) that exhibit activity relating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIFO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 61 AA;

Query Match 91.2%; Score 31; DB 4; Length 61;  
 Best Local Similarity 80.0%; Pred. No. 5.8e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 ||:|  
 Db 53 CHSVC 57

RESULT 82  
 AAY27620  
 ID AAY27620 standard; protein; 63 AA.  
 XX  
 AC AAY27620;

30-JUL-1999 (first entry)  
 Human secreted protein encoded by gene No. 54.

Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
 developmental abnormality; foetal deficiency; blood; allergy; renal;  
 immune system; asthma; lymphocytic disease; brain; hepatitis; lymphoma;  
 inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
 cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
 endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9924836-A1.  
 XX  
 PD 20-MAY-1999.  
 XX  
 PP 04-NOV-1998; 98WO-US023435.  
 XX  
 PR 07-NOV-1997; 97US-0064900P.  
 PR 07-NOV-1997; 97US-0064908P.  
 PR 07-NOV-1997; 97US-0064911P.  
 PR 07-NOV-1997; 97US-0064912P.  
 PR 07-NOV-1997; 97US-0064983P.  
 PR 07-NOV-1997; 97US-0064984P.  
 PR 07-NOV-1997; 97US-0064985P.  
 PR 07-NOV-1997; 97US-0064987P.  
 PR 07-NOV-1997; 97US-0064988P.  
 PR 17-NOV-1997; 97US-0066089P.  
 PR 17-NOV-1997; 97US-0066090P.  
 PR 17-NOV-1997; 97US-0066094P.  
 PR 17-NOV-1997; 97US-0066095P.  
 PR 17-NOV-1997; 97US-0066100P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Feng P, Carter KC, Endress GA, Rosen CA, Ruben SM, Janat F;  
 PI Ni J, Wei Y, Moore PA, Soppet DR, Kyaw H, Lafleur DW, Oleen HS;  
 PI Shi Y, Ebner R;  
 XX  
 DR WPI; 1999-337740/28.  
 DR N-PSDB; AAX84986.  
 XX  
 PT New human secreted proteins and coding sequences useful for treating  
 PT disorders of the immune system and hyperproliferative disorders.  
 XX  
 PS Claim 11; Page 381; 507pp; English.

This sequence represents a secreted human protein encoded by the gene  
 clone detailed in the descriptor line. The gene can be used to generate  
 fusion proteins by linking to the gene to a human immunoglobulin FC  
 portion (e.g. AAX84924) for increasing the stability of the fused protein  
 as compared to the human protein only. The invention relates to 125 novel  
 genes and their fragments (nucleic acid sequences: AAX84933-X85057; amino  
 acid sequences AAY27567-Y27933) which are useful for preventing, treating  
 or ameliorating medical conditions e.g. by protein or gene therapy. Also,  
 CC pathological conditions can be diagnosed by determining the amount of the  
 CC new polypeptides in a sample or by determining the presence of mutations  
 CC in the new polynucleotides. Specific uses are described for each of the  
 CC 125 polynucleotides, based on which tissues they are most highly  
 CC expressed in (see AAX84933 for described uses)

Query Match 91.2%; Score 31; DB 2; Length 63;  
 Best Local Similarity 80.0%; Pred. No. 5.9e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 ||:|

Db 19 CHSVC 23

RESULT 83  
AAM15142  
ID AAM15142 standard; protein; 63 AA.  
XX  
XX AAM15142;  
AC AAM15142;  
XX  
XX  
DT 12-OCT-2001 (first entry)  
XX  
XX Peptide #1576 encoded by probe for measuring cervical gene expression.  
DE  
XX Probe; human; microarray; gene expression; cervical epithelial cell;  
KW cervical cancer.  
XX  
XX  
OS Homo sapiens.  
XX  
XX WO200157278-A2.  
PN  
XX  
XX 09-AUG-2001.  
PD  
XX  
XX 30-JAN-2001; 2001WO-US000670.  
PF  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR  
XX 26-MAY-2000; 2000US-0207456P.  
PR  
XX 30-JUN-2000; 2000US-00608408.  
PR  
XX 03-AUG-2000; 2000US-00632366.  
PR  
XX 21-SEP-2000; 2000US-0234687P.  
PR  
XX 27-SEP-2000; 2000US-0236359P.  
PR  
XX 04-OCT-2000; 2000GB-00024263.  
PR  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI  
XX WPI; 2001-488901/53.  
DR  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human cervical epithelial cells.  
PT  
XX  
XX Claim 27; SEQ ID NO 19968; 487pp; English.  
PS  
XX The present invention relates to human single exon nucleic acid probes  
CC (SEN: see AAI10068-AA128459). The present sequence is a peptide encoded  
CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs  
CC can be used to produce a single exon microarray, which can be used for  
CC measuring human gene expression in a sample derived from human cervical  
CC epithelial cells. By measuring gene expression, the probes are therefore  
CC useful in grading and/or staging of diseases of the cervix, notably  
CC cervical cancer. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 63 AA;  
SQ

Query Match 91.2%; Score 31; DB 4; Length 63;  
Best Local Similarity 80.0%; Pred. No. 5.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
Db 36 CHALC 40

RESULT 84  
ABB34134  
ID ABB34134 standard; peptide; 63 AA.  
XX  
XX ABB34134;  
AC  
XX  
XX 04-FEB-2002 (first entry)  
DT  
XX

Query Match 91.2%; Score 31; DB 4; Length 63;  
Best Local Similarity 80.0%; Pred. No. 5.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
Db 36 CHALC 40

RESULT 85  
AAM27597  
ID AAM27597 standard; protein; 63 AA.  
XX  
XX AAM27597;  
AC  
XX  
XX 17-OCT-2001 (first entry)  
DT  
XX  
XX Peptide #1634 encoded by probe for measuring placental gene expression.  
DE  
XX Probe; microarray; human; placenta; antenatal diagnosis;  
KW genetic disorder.  
XX  
XX Homo sapiens.  
OS  
XX WO200157272-A2.  
PN  
XX  
XX 09-AUG-2001.  
PD  
XX  
XX 30-JAN-2001; 2001WO-US000663.  
PF  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR

DE Peptide #1640 encoded by human foetal liver single exon probe.  
XX  
KW Human; foetal liver; gene expression; single exon nucleic acid probe.  
XX  
OS Homo sapiens.  
XX  
XX WO200157277-A2.  
PN  
XX  
XX 09-AUG-2001.  
PD  
XX  
XX 30-JAN-2001; 2001WO-US000669.  
PF  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR  
XX 26-MAY-2000; 2000US-0207456P.  
PR  
XX 30-JUN-2000; 2000US-00608408.  
PR  
XX 03-AUG-2000; 2000US-00632366.  
PR  
XX 21-SEP-2000; 2000US-0234687P.  
PR  
XX 27-SEP-2000; 2000US-0236359P.  
PR  
XX 04-OCT-2000; 2000GB-00024263.  
PR  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI  
XX WPI; 2001-483447/52.  
DR  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human foetal liver.  
PT  
XX  
XX Claim 27; SEQ ID NO 26769; 639pp + Sequence Listing; English.  
PS  
XX The invention relates to a single exon nucleic acid probe for measuring  
CC human gene expression in a sample derived from human foetal liver. The  
CC single exon nucleic acid probes may be used for predicting, measuring and  
CC displaying gene expression in samples derived from human foetal liver. The  
CC present sequence is a peptide encoded by a single exon nucleic acid probe  
CC of the invention. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 63 AA;  
SQ

Query Match 91.2%; Score 31; DB 4; Length 63;  
Best Local Similarity 80.0%; Pred. No. 5.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
Db 36 CHALC 40

RESULT 85  
AAM27597  
ID AAM27597 standard; protein; 63 AA.  
XX  
XX AAM27597;  
AC  
XX  
XX 17-OCT-2001 (first entry)  
DT  
XX  
XX Peptide #1634 encoded by probe for measuring placental gene expression.  
DE  
XX Probe; microarray; human; placenta; antenatal diagnosis;  
KW genetic disorder.  
XX  
XX Homo sapiens.  
OS  
XX WO200157272-A2.  
PN  
XX  
XX 09-AUG-2001.  
PD  
XX  
XX 30-JAN-2001; 2001WO-US000663.  
PF  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR





XX ABG48967;  
AC  
XX  
DT 25-FEB-2003 (first entry)  
XX  
DE Human liver peptide, SEQ ID NO 27615.  
XX  
XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;  
KW hypercholesterolaemia; coronary heart disease.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200157273-A2.  
PN  
XX  
XX 09-AUG-2001.  
PD  
XX  
XX 30-JAN-2001; 2001WO-US0000564.  
PF  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR  
XX 26-MAY-2000; 2000US-0207456P.  
PR  
XX 30-JUN-2000; 2000US-00608408.  
PR  
XX 03-AUG-2000; 2000US-00632366.  
PR  
XX 21-SEP-2000; 2000US-0234687P.  
PR  
XX 27-SEP-2000; 2000US-0236359P.  
PR  
XX 04-OCT-2000; 2000GB-00024263.  
PR  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI  
XX WPI; 2001-488898/53.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human adult liver.  
PT  
XX  
XX Claim 27; SEQ ID NO 27615; 658pp; English.  
PS  
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for  
CC measuring human gene expression in a sample derived from human adult  
CC liver, comprising one of 13109 defined nucleotide sequences given in the  
CC specification (or complements/ fragments). The probe hybridises at high  
CC stringency to a nucleic acid molecule expressed in the human adult liver.  
CC (I) may be used for predicting, measuring and displaying gene expression  
CC in samples derived from human adult liver. The genes identified may be  
CC involved in genetic liver diseases such as cirrhosis.  
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is  
CC associated with coronary heart disease. ABG47348-ABG59930 represent human  
CC liver single exon encoded peptides of the invention. Note: The sequence  
CC information for this patent does not appear in the printed specification  
CC but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 63 AA;  
SQ  
Query Match 91.2%; Score 31; DB 4; Length 63;  
Best Local Similarity 80.0%; Pred. No. 5.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CHAVC 5  
Db 36 CHALC 40  
RESULT 91  
AA02883  
ID AA02883 standard; protein; 63 AA.  
XX  
XX  
AC AA02883;  
XX  
XX 09-OCT-2001 (first entry)  
DT  
XX Peptide #1565 encoded by probe for measuring breast gene expression.  
DE  
XX

KW Probe; human; breast disease; breast cancer; development disorder;  
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.  
XX  
OS Homo sapiens.  
XX  
XX WO200157270-A2.  
PN  
XX  
XX 09-AUG-2001.  
PD  
XX  
XX 29-JAN-2001; 2001WO-US0000661.  
PF  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR  
XX 26-MAY-2000; 2000US-0207456P.  
PR  
XX 30-JUN-2000; 2000US-00608408.  
PR  
XX 03-AUG-2000; 2000US-00632366.  
PR  
XX 21-SEP-2000; 2000US-0234687P.  
PR  
XX 27-SEP-2000; 2000US-0236359P.  
PR  
XX 04-OCT-2000; 2000GB-00024263.  
PR  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI  
XX WPI; 2001-476286/51.  
XX  
XX Novel single exon nucleic acid probe used to measuring gene expression in  
PT a human breast.  
PT  
XX  
XX Claim 27; SEQ ID NO 11623; 322pp; English.  
PS  
XX The present invention relates to novel single exon nucleic acid probes  
CC (see AA100010-AA110067). The present sequence is a peptide encoded by one  
CC such probe. The probes are useful for measuring human gene expression in  
CC a human breast sample, where the probe hybridises at high stringency to a  
CC nucleic acid expressed in the human breast. The probes are useful for  
CC predicting, diagnosing, grading, staging, monitoring and prognosing  
CC diseases of the human breast, particularly those diseases with polygenic  
CC aetiology. The diseases include: breast cancer, disorders of development,  
CC inflammatory diseases of the breast, fibrocystic changes, proliferative  
CC breast disease and non-carcinoma tumours. Note: The sequence data for  
CC this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 63 AA;  
SQ  
Query Match 91.2%; Score 31; DB 4; Length 63;  
Best Local Similarity 80.0%; Pred. No. 5.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CHAVC 5  
Db 36 CHALC 40  
RESULT 92  
ABG36952  
ID ABG36952 standard; peptide; 63 AA.  
XX  
XX  
AC ABG36952;  
XX  
XX 19-AUG-2002 (first entry)  
DT  
XX  
XX Human peptide encoded by genome-derived single exon probe SEQ ID 26617.  
DE  
XX  
XX Human; single exon probe; asthma; lung cancer; COPD; ILD;  
KW chronic obstructive pulmonary disease; interstitial lung disease;  
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
KW tuberculous sclerosis; Gaucher's disease; Niemann-Pick disease;  
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
KW primary ciliary dyskinesia; pulmonary hypertension;



DT 24-OCT-2001 (first entry)  
 XX Human novel protein #290.  
 DE  
 XX Human; novel protein; Antianaemic; osteopathic; antiinflammatory;  
 XX immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;  
 KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;  
 KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;  
 KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;  
 KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;  
 KW tissue regeneration; immune disorder.  
 XX  
 OS Homo sapiens.  
 XX WO200155437-A2.  
 XX  
 PN 02-AUG-2001.  
 XX  
 XX 25-JAN-2001; 2001WO-US002623.  
 XX  
 XX 25-JAN-2000; 2000US-00491404.  
 XX (HYSE-) HYSEQ INC.  
 PA  
 XX Tang YT, Liu C, Drmanac RT;  
 FI  
 XX WPI; 2001-451939/48.  
 XX N-PSDB; RAS22724.  
 DR  
 XX Isolated polypeptides useful for treating anti-inflammatory diseases,  
 PT nervous system disorders, and for regenerating bone and cartilage.  
 PT  
 XX Example 4; Page 808; 894pp; English.  
 PS  
 XX The invention relates to polynucleotides encoding novel human proteins or  
 CC their active domains. The polypeptides, polynucleotides and antibodies  
 CC raised against the polypeptides are used in a method of treatment of a  
 CC mammal and prevention of disorders caused by the aberrant protein  
 CC expression or activity. The polypeptides can be used as molecular weight  
 CC markers, food supplements, and in antibody production. The polypeptides  
 CC are used to identify compounds which bind to the polypeptides.  
 CC Polynucleotides of the invention are used as probes and primers, for  
 CC sequencing, for chromosome or gene mapping, in the production of  
 CC recombinant proteins, and in generating anti-sense DNA or RNA and in gene  
 CC therapy. Polypeptides of the invention can be used to target drugs to a  
 CC tumour, in assays to determine biological activity, to raise  
 CC antibodies/ elicit an immune response, to determine quantitative protein  
 CC levels, as tissue markers, and to isolate receptors or ligands.  
 CC Polypeptides of the invention may also be useful in treating platelet  
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,  
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting  
 CC the proliferation, differentiation and survival of stem cells, as a  
 CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,  
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral  
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or  
 CC fungal infection or from autoimmunity, cancer, allergy, asthma, graft-  
 CC versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory  
 CC diseases, nervous system disorders, and infection. The present sequence  
 CC represents a protein of the invention  
 XX  
 SQ Sequence 96 AA;  
 Query Match 91.2%; Score 31; DB 4; Length 96;  
 Best Local Similarity 80.0%; Pred. No. 8.5e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CHAVC 5  
 Db 81 CHSVC 85  
 ||:|  
 RESULT 95  
 ADH80737

ID ADH80737 standard; protein; 96 AA.  
 XX ADH80737;  
 AC  
 XX 22-APR-2004 (first entry)  
 DT Human polypeptide #54.  
 XX  
 DE Human; coagulation disorder; haemophilia; wound; stroke; thrombosis;  
 KW myocardial infarction; cancer; bone fracture; Alzheimer's disease;  
 KW Parkinson's disease; autoimmune disorder; food supplement; haemostatic;  
 KW vulnerary; cerebroprotective; thrombolytic; anticoagulant; cardiant;  
 KW cytostatic; osteopathic; neuroprotective; nootropic; antiparkinsonian;  
 KW immunosuppressive.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003232054-A1.  
 XX  
 XX 18-DEC-2003.  
 PD  
 XX  
 XX 08-NOV-2002; 2002US-00291265.  
 PF  
 XX 25-JAN-2000; 2000US-00491404.  
 XX 17-JUL-2000; 2000US-00617746.  
 PR 03-AUG-2000; 2000US-00631451.  
 PR 15-SEP-2000; 2000US-00663870.  
 PR 25-JAN-2001; 2001WO-US002623.  
 PR 03-AUG-2001; 2001US-00922279.  
 XX (TANG/) TANG Y T.  
 PA (LIUC/) LIU C.  
 PA (ASUN/) ASUNDI V.  
 PA (CHEN/) CHEN R.  
 PA (QIAN/) QIAN X B.  
 PA (WANG/) WANG Z W.  
 PA (WEHR/) WEHRMAN T.  
 PA (ZHAN/) ZHANG J.  
 PA (ZHOU/) ZHOU P.  
 PA (CAOY/) CAO Y.  
 PA (DRMA/) DRMANAC R T.  
 XX  
 XX Tang YT, Liu C, Aeundi V, Chen R, Qian XB, Wang ZW, Wehrman T;  
 FI Zhang J, Zhou P, Cao Y, Drmanac RT;  
 XX  
 XX WPI; 2004-061257/06.  
 DR  
 XX New polynucleotides and polypeptides useful for diagnosing, preventing or  
 PT treating diseases involving aberrant protein expression or activity, e.g.  
 PT hemophilia, wounds, stroke, thrombosis, cancer or autoimmune disorders.  
 XX  
 PS Claim 20; SEQ ID NO 762; 85pp; English.  
 XX The invention relates to new isolated polynucleotides and polypeptides.  
 CC The sequences, compositions and methods of the invention are useful for  
 CC diagnosing, preventing or treating diseases involving aberrant protein  
 CC expression or biological activity, such as coagulation disorders (e.g.  
 CC haemophilia), wounds, stroke, thrombosis, myocardial infarction, cancer,  
 CC bone fractures, Alzheimer's disease, Parkinson's disease and autoimmune  
 CC disorders. The polynucleotides may be used as hybridization probes, as  
 CC oligomers or primers, for polymerase chain reaction, for chromosome and  
 CC gene mapping, in the recombinant production of proteins and in generating  
 CC of antisense DNA or RNA. The polypeptides may be used in generating  
 CC antibodies, as molecular weight markers or as food supplements. This  
 CC sequence represents a human polypeptide of the invention.  
 XX  
 SQ Sequence 96 AA;  
 Query Match 91.2%; Score 31; DB 8; Length 96;  
 Best Local Similarity 80.0%; Pred. No. 8.5e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CHAVC 5

```
Db      81 CHSVC 85
||:|
RESULT 96
ADO34044
ID ADO34044 standard; protein; 100 AA.
XX
AC ADO34044;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human CLA2.3, SEQ ID 7.
XX
KW Cytostatic; human; Colorectal Lesion Associated 2; CLA2; chromosome 5p14;
KW proliferative disorder; tumour; cancer; carcinoma; dysplasia.
XX
OS Homo sapiens.
XX
PN EPI426442-A1.
XX
PD 09-JUN-2004.
XX
PF 02-DEC-2002; 2002EP-00026772.
XX
PR 02-DEC-2002; 2002EP-00026772.
XX
PA (MTM-) MTM LAB AG.
XX
PI Hipfel R;
XX
DR WPI; 2004-422595/40.
DR N-PSDB; ADO34043.
XX
PT New isolated colorectal lesion associated nucleic acid molecule useful in
PT the detection and therapy of proliferative disorders.
PS Claim 6; SEQ ID NO 7; 123pp; English.
XX
CC The present invention relates to the human Colorectal Lesion Associated 2
CC (CLA2) gene (I; ADO34038), which is located on chromosome 5p14. CLA2
CC sequences are useful for the detection and treatment of proliferative
CC disorders such as: a benign and malignant tumour (head, neck, respiratory
CC tract, gastrointestinal tract, skin and its appendages, central and
CC peripheral nervous system, urinary system, reproductive system, endocrine
CC system, soft tissues and bone, lymphopoietic and haematopoietic system,
CC breast, anogenital or colorectal cancers), a carcinoma or a dysplasia.
CC The present sequence was used to illustrate the invention.
XX
SQ Sequence 100 AA;

Query Match 91.2%; Score 31; DB 8; Length 100;
Best Local Similarity 80.0%; Pred. No. 8.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 85 CHALC 89
|||:|

RESULT 97
ADM05223
ID ADM05223 standard; protein; 117 AA.
XX
AC ADM05223;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human protein of the invention SEQ ID NO:3908.
XX
KW human; gene therapy; diagnostic marker; pharmaceutical.
XX
OS Homo sapiens.

XX PN EPI1347046-A1.
XX
PD 24-SEP-2003.
XX
PF 12-APR-2002; 2002EP-00008400.
XX
PR 22-MAR-2002; 2002JP-00137785.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-723558/69.
DR N-PSDB; ADM02780.
XX
PT New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
PS Claim 1; SEQ ID NO 3908; 305pp; English.
XX
CC The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC protein sequence of the invention.
XX
SQ Sequence 117 AA;

Query Match 91.2%; Score 31; DB 7; Length 117;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 74 CHALC 78
|||:|

RESULT 98
ABG05990
ID ABG05990 standard; protein; 134 AA.
XX
AC ABG05990;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #5981.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
```



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XX WPI; 2001-639362/73.
DR N-PSDB; RAS70177.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
FT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 36349; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have application in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 134 AA;
SQ
Query Match 91.2%; Score 31; DB 4; Length 134;
Best Local Similarity 80.0%; Pred. NO. 1.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CHAVC 5
Db 90 CHALC 94
|||:|
|:|:|

RESULT 99
ADM26297
ID ADM26297 standard; protein; 139 AA.
XX
AC ADM26297;
XX
DT 20-MAY-2004 (first entry)
XX
DE Hyperthermophile Methanopyrus kandleri protein #903.
XX
KW hyperthermophile; protein stability enhancement;
XX protein activity enhancement.
XX
OS Methanopyrus kandleri.
XX
PN WO2003076575-A2.
XX
PD 18-SEP-2003.
XX
PF 04-MAR-2003; 2003WO-US006664.
XX
PR 04-MAR-2002; 2002US-0361742P.
XX
PR 14-MAY-2002; 2002US-0380423P.
XX
PR 16-SEP-2002; 2002US-0410974P.
XX
XX (FIDE-) FIDELITY SYSTEMS INC.
PA (MALY/) MALYKH A.
XX
PI Slesarev AI, Pavlov A, Pavlova N, Kozyavkin S;

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XX WPI; 2003-748383/70.
DR N-PSDB; ADM27081.
XX
PT New isolated nucleic acids encoding any of about 1700 Methanopyrus
FT kandleri proteins, and the encoded proteins, useful as a medicaments or
PT as diagnostic agents.
XX
PS Claim 31; SEQ ID NO 903; 1023pp; English.
XX
CC The invention comprises the amino acid sequence of proteins from the
CC hyperthermophile Methanopyrus kandleri, the invention also comprises the
CC complete genome from Methanopyrus kandleri. The Methanopyrus kandleri
CC proteins of the invention are useful for enhancing the stability and/or
CC activity of other proteins. The Methanopyrus kandleri genome is useful in
CC a variety of diagnostic and analytical methods. The present amino acid
CC sequence represents a Methanopyrus kandleri protein of the invention.
XX
SQ Sequence 139 AA;
Query Match 91.2%; Score 31; DB 7; Length 139;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CHAVC 5
Db 91 CHSVC 95
|||:|
|:|:|

RESULT 100
ABJ18656
ID ABJ18656 standard; protein; 148 AA.
XX
AC ABJ18656;
XX
DT 20-FEB-2003 (first entry)
XX
DE Human erbB receptor subdomain IV protein #1.
XX
KW Human; vaccine; erbB receptor antagonist; tumour; cancer; gastric cancer;
XX breast cancer; prostate cancer; erbB receptor subdomain IV.
XX
OS Homo sapiens.
XX
PN WO200281649-A2.
XX
PD 17-OCT-2002.
XX
PF 08-APR-2002; 2002WO-US011211.
XX
PR 06-APR-2001; 2001US-0282037P.
XX
PR 03-AUG-2001; 2001US-0309864P.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
PI Greene MI, Zhang H, Murali R, Richter M, Berezov A, Liu Q;
XX Chen J;
XX
XX WPI; 2003-075482/07.
XX
XX New peptide antagonists against erbB receptors, useful for preventing or
XX treating tumors or cancers (e.g. lung adenocarcinomas, breast carcinomas
XX or prostate cancer) in humans.
XX
PS Claim 46; Page 110-111; 115pp; English.
XX
CC The invention comprises peptide antagonists designed to target erbB
XX receptors. The erbB receptor peptide antagonists are useful for
XX preventing tumours and cancers (e.g. gastric cancer, breast cancer and
XX prostate cancer). The present amino acid sequence represents a human erbB
XX subdomain IV protein
XX
XX Sequence 148 AA;

```

Query Match 91.2%; Score 31; DB 6; Length 148;  
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
 |||:  
 Db 3 CHALC 7

Search completed: July 26, 2005, 23:58:04  
 Job time : 168 secs

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OM protein - protein search, using sw model

Run on: July 26, 2005, 23:52:35 ; Search time 41 Seconds  
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Title: US-10-632-678-10  
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Sequence: 1 CHAVC 5

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	5	3	US-08-893-534A-8
2	34	100.0	5	3	US-08-996-679-8
3	34	100.0	5	3	US-09-115-395-10
4	34	100.0	5	3	US-09-102-540-15175
5	34	100.0	5	3	US-09-250-059-10
6	34	100.0	5	3	US-09-248-074-10
7	34	100.0	5	4	US-09-357-717-10
8	34	100.0	5	4	US-09-458-870-10
9	34	100.0	5	4	US-09-057-363C-22
10	34	100.0	5	4	US-09-057-363C-34
11	34	100.0	5	4	US-09-248-015-10
12	34	100.0	5	4	US-09-544-782-10
13	34	100.0	5	4	US-09-234-395-296
14	34	100.0	5	4	US-09-305-928-296
15	34	100.0	5	4	US-09-265-107-22
16	34	100.0	5	4	US-09-265-107-34
17	34	100.0	5	4	US-10-058-821-10
18	34	100.0	6	4	US-09-458-870-84
19	34	100.0	6	4	US-09-458-870-87
20	34	100.0	6	4	US-09-458-870-88
21	34	100.0	6	4	US-09-458-870-91
22	34	100.0	6	4	US-09-458-870-92
23	34	100.0	6	4	US-09-458-870-93
24	34	100.0	6	4	US-09-458-870-100
25	34	100.0	6	4	US-09-544-782-54
26	34	100.0	6	4	US-09-544-782-84
27	34	100.0	6	4	US-09-544-782-87

28	34	100.0	6	4	US-09-544-782-88	Sequence 88, Appl
29	34	100.0	6	4	US-09-544-782-91	Sequence 91, Appl
30	34	100.0	6	4	US-09-544-782-92	Sequence 92, Appl
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32	34	100.0	7	4	US-09-458-870-89	Sequence 89, Appl
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35	34	100.0	7	4	US-09-544-782-89	Sequence 89, Appl
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38	34	100.0	8	4	US-09-458-870-95	Sequence 95, Appl
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40	34	100.0	8	4	US-09-544-782-95	Sequence 95, Appl
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42	33	97.1	163	4	US-09-949-016-10680	Sequence 10680, A
43	31	91.2	257	4	US-09-543-681A-7794	Sequence 7794, Ap
44	31	91.2	312	3	US-09-210-637-34	Sequence 34, Appl
45	31	91.2	313	3	US-09-347-878-30	Sequence 30, Appl
46	31	91.2	313	4	US-09-367-007C-39	Sequence 39, Appl
47	31	91.2	339	4	US-09-949-016-10160	Sequence 10160, A
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50	31	91.2	1210	2	US-08-484-438-7	Sequence 7, Appl
51	31	91.2	1210	2	US-08-475-035-4	Sequence 4, Appl
52	31	91.2	1210	4	US-09-715-249-2	Sequence 2, Appl
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54	30	88.2	5	3	US-08-996-679-9	Sequence 9, Appl
55	30	88.2	5	3	US-09-115-395-20	Sequence 20, Appl
56	30	88.2	5	3	US-09-507-102-9	Sequence 9, Appl
57	30	88.2	5	3	US-09-250-059-11	Sequence 11, Appl
58	30	88.2	5	3	US-09-248-074-11	Sequence 11, Appl
59	30	88.2	5	4	US-09-357-717-11	Sequence 11, Appl
60	30	88.2	5	4	US-09-458-870-11	Sequence 11, Appl
61	30	88.2	5	4	US-09-248-015-20	Sequence 20, Appl
62	30	88.2	5	4	US-09-544-782-11	Sequence 11, Appl
63	30	88.2	5	4	US-10-058-821-11	Sequence 11, Appl
64	30	88.2	16	4	US-09-910-009A-358	Sequence 358, App
65	30	88.2	16	4	US-09-910-009A-454	Sequence 454, App
66	30	88.2	17	3	US-08-331-625A-35	Sequence 35, Appl
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72	30	88.2	165	4	US-09-270-767-55116	Sequence 55116, A
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79	30	88.2	374	2	US-07-857-224B-85	Sequence 85, Appl
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82	30	88.2	1101	3	US-08-331-625A-52	Sequence 52, Appl
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91	30	88.2	1452	5	PCT-US93-04692-2	Sequence 2, Appl
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94	30	88.2	1454	4	US-09-854-799-22	Sequence 22, Appl
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97	30	88.2	1454	5	PCT-US91-08525-26	Sequence 26, Appl
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99	30	88.2	1454	5	PCT-US93-04384-8	Sequence 8, Appl
100	30	88.2	1454	5	PCT-US93-04384-16	Sequence 16, Appl

## ALIGNMENTS

RESULT 1  
US-08-893-534A-8  
; Sequence 8, Application US/08893534A  
; Patent No. 6031072  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: CELL ADHESION  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/893,534A  
; FILING DATE: 11-JUL-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 100086.401  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: circular  
; MOLECULE TYPE: peptide  
US-08-893-534A-8  
  
Query Match 100.0%; Score 34; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CHAVC 5  
Db 1 CHAVC 5  
  
RESULT 2  
US-08-996-679-8  
; Sequence 8, Application US/08996679  
; Patent No. 6169071  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: CELL ADHESION  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/996,679  
; FILING DATE: 23-DEC-1997  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 100086.401C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: circular  
; MOLECULE TYPE: peptide  
US-08-996-679-8  
  
Query Match 100.0%; Score 34; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 CHAVC 5  
  
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; Sequence 10, Application US/09115395A  
; Patent No. 6207639  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NEURITE OUTGROWTH  
; FILE REFERENCE: 100086.401C3  
; CURRENT APPLICATION NUMBER: US/09/115,395A  
; CURRENT FILING DATE: 1998-07-14  
; EARLIER APPLICATION NUMBER: 08/996,679  
; EARLIER FILING DATE: 1997-12-23  
; EARLIER APPLICATION NUMBER: 08/893,534  
; EARLIER FILING DATE: 1997-07-11  
; EARLIER APPLICATION NUMBER: 60/021,612  
; EARLIER FILING DATE: 1996-07-12  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase  
; OTHER INFORMATION: Synthesis  
US-09-115-395-10  
  
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Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CHAVC 5  
Db 1 CHAVC 5  
  
RESULT 4  
US-09-507-102-8

; Sequence 8, Application US/09507102  
; Patent No. 6326352  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; CELL ADHESION  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED IP LAW GROUP PLLC  
; STREET: 6300 Bank of America Bldg., 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/507,102  
; FILING DATE: 17-Feb-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/893,534  
; FILING DATE: 11-JUL-1997  
; APPLICATION NUMBER: US 60/021,612  
; FILING DATE: 12-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Christiansen, William T.  
; REGISTRATION NUMBER: 44,614  
; REFERENCE/DOCKET NUMBER: 100086.401C10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: circular  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-09-507-102-8

Query Match 100.0%; Score 34; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CHAVC 5  
Db 1 CHAVC 5

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; Sequence 10, Application US/09250059  
; Patent No. 6333307  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NEURITE OUTGROWTH  
; FILE REFERENCE: 100086.401C6  
; CURRENT APPLICATION NUMBER: US/09/250,059  
; CURRENT FILING DATE: 1999-02-12  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-09-250-059-10

Query Match 100.0%; Score 34; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
Db 1 CHAVC 5

RESULT 6  
US-09-248-074-10  
; Sequence 10, Application US/09248074  
; Patent No. 6346512  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401C5  
; CURRENT APPLICATION NUMBER: US/09/248,074  
; CURRENT FILING DATE: 1999-02-10  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-09-248-074-10

Query Match 100.0%; Score 34; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
Db 1 CHAVC 5

RESULT 7  
US-09-357-717-10  
; Sequence 10, Application US/09357717  
; Patent No. 6417325  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR CANCER THERAPY  
; FILE REFERENCE: 100086.401C7  
; CURRENT APPLICATION NUMBER: US/09/357,717  
; CURRENT FILING DATE: 1999-07-20  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

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; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-357-717-10

Query Match          100.0%; Score 34; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 CHAVC 5

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US-09-458-870-10
; Sequence 10, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C8
; CURRENT APPLICATION NUMBER: US/09/458,870
; CURRENT FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-458-870-10

Query Match          100.0%; Score 34; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
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Db      1 CHAVC 5

RESULT 9
US-09-057-363C-22
; Sequence 22, Application US/09057363C
; Patent No. 6551994
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE
; INTERACTION BETWEEN ALPHA-CATENIN AND BETA-CATENIN
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,363C
; FILING DATE: 08-Apr-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Christiansen, William T.
; REGISTRATION NUMBER: 44,614
; REFERENCE/DOCKET NUMBER: 100086.406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-057-363C-22

Query Match          100.0%; Score 34; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
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Db      1 CHAVC 5

RESULT 10
US-09-057-363C-34
; Sequence 34, Application US/09057363C
; Patent No. 6551994
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE
; INTERACTION BETWEEN ALPHA-CATENIN AND BETA-CATENIN
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,363C
; FILING DATE: 08-Apr-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Christiansen, William T.
; REGISTRATION NUMBER: 44,614
; REFERENCE/DOCKET NUMBER: 100086.406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: circular
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Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 CHAVC 5
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RESULT 11
US-09-248-015-10
; Sequence 10, Application US/09248015
; Patent No. 6562786
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING APOPTOSIS
; FILE REFERENCE: 100086.401C4
; CURRENT APPLICATION NUMBER: US/09/248.015
; CURRENT FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-248-015-10
Query Match      100.0%; Score 34; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      1 CHAVC 5
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RESULT 12
US-09-544-782-10
; Sequence 10, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Amar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9
; CURRENT APPLICATION NUMBER: US/09/544.782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-544-782-10
Query Match      100.0%; Score 34; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      1 CHAVC 5
      |||||

RESULT 13
US-09-234-395-296
; Sequence 296, Application US/09234395
; Patent No. 6680175
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER
; FILE REFERENCE: 100086.407C2
; CURRENT APPLICATION NUMBER: US/09/234.395
; CURRENT FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 296
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Synthesis and Cyclization based on Human
; OTHER INFORMATION: N-Cadherin
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-234-395-296
Query Match      100.0%; Score 34; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      1 CHAVC 5
      |||||

RESULT 14
US-09-305-928-296
; Sequence 296, Application US/09305928
; Patent No. 6682901
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER
; FILE REFERENCE: 100086.407C4
; CURRENT APPLICATION NUMBER: US/09/305.928
; CURRENT FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 296
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Synthesis and Cyclization based on Human
; OTHER INFORMATION: N-Cadherin
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-305-928-296
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RESULT 19  
US-09-458-870-87  
; Sequence 87, Application US/09458870  
; Patent No. 6465427  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Ammar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401C8  
; CURRENT APPLICATION NUMBER: US/09/458,870  
; CURRENT FILING DATE: 1999-12-10  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 87  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-09-458-870-87  
Query Match 100.0%; Score 34; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CHAVC 5  
Db 1 CHAVC 5  
|||||

RESULT 20  
US-09-458-870-88  
; Sequence 88, Application US/09458870  
; Patent No. 6465427  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Ammar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401C8  
; CURRENT APPLICATION NUMBER: US/09/458,870  
; CURRENT FILING DATE: 1999-12-10  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 88  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-09-458-870-88  
Query Match 100.0%; Score 34; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CHAVC 5  
Db 1 CHAVC 5  
|||||

RESULT 21  
US-09-458-870-91  
; Sequence 91, Application US/09458870  
; Patent No. 6465427  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Ammar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401C8  
; CURRENT APPLICATION NUMBER: US/09/458,870  
; CURRENT FILING DATE: 1999-12-10  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 91  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-09-458-870-91  
Query Match 100.0%; Score 34; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CHAVC 5  
Db 1 CHAVC 5  
|||||

RESULT 22  
US-09-458-870-92  
; Sequence 92, Application US/09458870  
; Patent No. 6465427  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Ammar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401C8  
; CURRENT APPLICATION NUMBER: US/09/458,870  
; CURRENT FILING DATE: 1999-12-10  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 92  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-09-458-870-92  
Query Match 100.0%; Score 34; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CHAVC 5  
Db 1 CHAVC 5  
|||||

```

QY      1 CHAVC 5
      |||||
Db      1 CHAVC 5

RESULT 23
US-09-458-870-93
; Sequence 93, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C8
; CURRENT APPLICATION NUMBER: US/09/458,870
; CURRENT FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-458-870-93

Query Match      100.0%; Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
      |||||
Db      1 CHAVC 5

RESULT 24
US-09-458-870-100
; Sequence 100, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C8
; CURRENT APPLICATION NUMBER: US/09/458,870
; CURRENT FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 100
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-458-870-100

Query Match      100.0%; Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
      |||||
Db      1 CHAVC 5

RESULT 25
US-09-544-782-54
; Sequence 54, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9
; CURRENT APPLICATION NUMBER: US/09/544,782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-544-782-54

Query Match      100.0%; Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
      |||||
Db      2 CHAVC 6

RESULT 26
US-09-544-782-84
; Sequence 84, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9
; CURRENT APPLICATION NUMBER: US/09/544,782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-544-782-84

Query Match      100.0%; Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
      |||||
Db      2 CHAVC 6

RESULT 27
US-09-544-782-84
; Sequence 84, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9
; CURRENT APPLICATION NUMBER: US/09/544,782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-544-782-84
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Query Match 100.0%; Score 34; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|  
|  
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|  
|  
Db 1 CHAVC 5

RESULT 27  
US-09-544-782-87  
; Sequence 87, Application US/09544782  
; Patent No. 6610821  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Ammar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401C9  
; CURRENT APPLICATION NUMBER: US/09/544,782  
; CURRENT FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 87  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-09-544-782-87

Query Match 100.0%; Score 34; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|  
|  
|  
|  
|  
Db 1 CHAVC 5

RESULT 28  
US-09-544-782-88  
; Sequence 88, Application US/09544782  
; Patent No. 6610821  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Ammar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401C9  
; CURRENT APPLICATION NUMBER: US/09/544,782  
; CURRENT FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 88  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group

US-09-544-782-88

Query Match 100.0%; Score 34; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|  
|  
|  
|  
|  
Db 2 CHAVC 6

RESULT 29  
US-09-544-782-91  
; Sequence 91, Application US/09544782  
; Patent No. 6610821  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Ammar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401C9  
; CURRENT APPLICATION NUMBER: US/09/544,782  
; CURRENT FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 91  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-09-544-782-91

Query Match 100.0%; Score 34; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|  
|  
|  
|  
|  
Db 1 CHAVC 5

RESULT 30  
US-09-544-782-92  
; Sequence 92, Application US/09544782  
; Patent No. 6610821  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Ammar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401C9  
; CURRENT APPLICATION NUMBER: US/09/544,782  
; CURRENT FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 92  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group

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; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-544-782-92
Query Match 100.0%; Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CHAVC 5
Db 1 CHAVC 5
RESULT 31
US-09-544-782-93
; Sequence 93, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9
; CURRENT APPLICATION NUMBER: US/09/544,782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-544-782-93
Query Match 100.0%; Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CHAVC 5
Db 1 CHAVC 5
RESULT 32
US-09-458-870-89
; Sequence 89, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C8
; CURRENT APPLICATION NUMBER: US/09/458,870
; CURRENT FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-458-870-89
Query Match 100.0%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CHAVC 5
Db 2 CHAVC 6
RESULT 33
US-09-458-870-90
; Sequence 90, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C8
; CURRENT APPLICATION NUMBER: US/09/458,870
; CURRENT FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-458-870-90
Query Match 100.0%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CHAVC 5
Db 2 CHAVC 6
RESULT 34
US-09-458-870-96
; Sequence 96, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C8
; CURRENT APPLICATION NUMBER: US/09/458,870
; CURRENT FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 96
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
```

; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-09-458-870-96

Query Match 100.0%; Score 34; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|  
|  
|  
|  
Db 3 CHAVC 7

RESULT 35  
US-09-544-782-89  
; Sequence 89, Application US/09544782  
; Patent No. 6610821  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Ammar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401C9  
; CURRENT APPLICATION NUMBER: US/09/544,782  
; CURRENT FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 89  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-09-544-782-89

Query Match 100.0%; Score 34; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|  
|  
|  
|  
Db 1 CHAVC 5

RESULT 36  
US-09-544-782-90  
; Sequence 90, Application US/09544782  
; Patent No. 6610821  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Ammar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401C9  
; CURRENT APPLICATION NUMBER: US/09/544,782  
; CURRENT FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 90  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-09-544-782-90

Query Match 100.0%; Score 34; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|  
|  
|  
|  
Db 2 CHAVC 6

RESULT 37  
US-09-544-782-96  
; Sequence 96, Application US/09544782  
; Patent No. 6610821  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Ammar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401C9  
; CURRENT APPLICATION NUMBER: US/09/544,782  
; CURRENT FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 96  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-09-544-782-96

Query Match 100.0%; Score 34; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|  
|  
|  
|  
Db 3 CHAVC 7

RESULT 38  
US-09-458-870-95  
; Sequence 95, Application US/09458870  
; Patent No. 6465427  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Ammar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401C8  
; CURRENT APPLICATION NUMBER: US/09/458,870  
; CURRENT FILING DATE: 1999-12-10  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 95  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-458-870-95

Query Match      100.0%; Score 34; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
   |||||
Db 3 CHAVC 7

RESULT 39
US-09-458-870-101
; Sequence 101, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Annmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C8
; CURRENT APPLICATION NUMBER: US/09/458,870
; CURRENT FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
; NAME/KEY: MOD RES
; LOCATION: (5)
; OTHER INFORMATION: Where Xaa is beta,beta-dimethyl cysteine
US-09-458-870-101

Query Match      100.0%; Score 34; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
   |||||
Db 3 CHAVC 7

RESULT 40
US-09-544-782-95
; Sequence 95, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Annmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9

; CURRENT APPLICATION NUMBER: US/09/544,782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-544-782-95

Query Match      100.0%; Score 34; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
   |||||
Db 3 CHAVC 7

RESULT 41
US-08-311-731A-213
; Sequence 213, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSES: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 213:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 542 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium leprae
US-08-311-731A-213

Query Match      100.0%; Score 34; DB 4; Length 542;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
```

```
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
   |||||
Db 1 CHAVC 5

RESULT 42
US-09-949-016-10680
; Sequence 10680, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10680
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10680

Query Match 97.1%; Score 33; DB 4; Length 163;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
   |||||
Db 65 CHAIC 69

RESULT 43
US-09-543-681A-7794
; Sequence 7794, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7794
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7794

Query Match 91.2%; Score 31; DB 4; Length 257;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
   |||||
Db 32 CHALC 36

RESULT 44
US-09-230-637-34
; Sequence 34, Application US/09230637
```

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; Patent No. 6264958
; GENERAL INFORMATION:
; APPLICANT: Hayward, Gary
; APPLICANT: Nicholas, John
; APPLICANT: Hardwick, J. Marie
; APPLICANT: Reitz, Marvin
; TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma
Associated Herpesvirus
; FILE REFERENCE: 1107.78372
; CURRENT APPLICATION NUMBER: US/09/230,637
; CURRENT FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/022,591
; PRIOR FILING DATE: 1996-07-25
; PRIOR APPLICATION NUMBER: PCT US 97/12931
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-230-637-34

Query Match 91.2%; Score 31; DB 3; Length 312;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
   |||||
Db 194 CHALC 198

RESULT 45
US-09-347-878-30
; Sequence 30, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:
; APPLICANT: Yuan, Chong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
; FILE REFERENCE: 25885-1651
; CURRENT APPLICATION NUMBER: US/09/347,878C
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human thymidylate synthase protein sequence
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: D00596/GenBank
US-09-347-878-30

Query Match 91.2%; Score 31; DB 3; Length 313;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
   |||||
Db 195 CHALC 199

RESULT 46
US-09-367-007C-39
; Sequence 39, Application US/09367007C
; Patent No. 6416987
; GENERAL INFORMATION:
; APPLICANT: Bertino, Joseph R.
; APPLICANT: Banerjee, Debabrata
; APPLICANT: Tong, Youzhi
; APPLICANT: Liu-Chen, Xinyue
; TITLE OF INVENTION: Mutants of Thymidylate Synthase and Uses Thereof
```

```
; FILE REFERENCE: D5978
; CURRENT APPLICATION NUMBER: US/09/367,007C
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/US98/02145
; PRIOR FILING DATE: 1998-01-03
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 39
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Wild type human thymidylate synthase amino acid
; OTHER INFORMATION: sequence (Genbank Accession number NP001062)
US-09-367-007C-39

Query Match          91.2%; Score 31; DB 4; Length 313;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      195 CHALC 199

RESULT 47
US-09-949-016-10160
; Sequence 10160, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 10160
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10160

Query Match          91.2%; Score 31; DB 4; Length 339;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      221 CHALC 225

RESULT 48
US-08-336-708A-9
; Sequence 9, Application US/08336708A
; Patent No. 5521295
; GENERAL INFORMATION:
; APPLICANT: Pacifici, Robert E.
; APPLICANT: Thomason, Arlen R.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Hybrid Receptor Molecules
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
```

```
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,708A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oleski, Nancy
; REFERENCE/DOCKET NUMBER: A-241A
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 644 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-336-708A-9

Query Match          91.2%; Score 31; DB 1; Length 644;
Best Local Similarity 80.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      506 CHALC 510

RESULT 49
US-09-328-352-7293
; Sequence 7293, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7293
; LENGTH: 760
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7293

Query Match          91.2%; Score 31; DB 4; Length 760;
Best Local Similarity 80.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      3 CHALC 7

RESULT 50
US-08-484-438-7
; Sequence 7, Application US/08484438
; Patent No. 5811098
; Patent No. 5811098 5780031
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory D.
; APPLICANT: Culouscou, Jean-Michel
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Siegall, Clay B.
; APPLICANT: Hellstr m, Ingegerd
; APPLICANT: Hellstr m, Karl E.
; TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
; NUMBER OF SEQUENCES: 42
```



```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,438
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/323,442
; FILING DATE: 14-OCT-1994
; APPLICATION NUMBER: US 08/150,704
; FILING DATE: 10-NOV-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/981,165
; FILING DATE: 24-NOV-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-230
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1210 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-484-438-7

Query Match 91.2%; Score 31; DB 2; Length 1210;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 506 CHALC 510

RESULT 51
US-08-475-035-4
; Sequence 4, Application US/08475035
; Patent No. 5985553
; GENERAL INFORMATION:
; APPLICANT: KING, C. R.
; APPLICANT: KRAUS, MATTHIAS H.
; APPLICANT: AARONSON, STUART A.
; TITLE OF INVENTION: HUMAN GENE RELATED TO BUT DISTINCT FROM
; TITLE OF INVENTION: EGF RECEPTOR GENE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,035
; FILING DATE: 7 Jun 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Peirymann, David G.
; REGISTRATION/DOCKET NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.656
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-475-035-4

Query Match 91.2%; Score 31; DB 2; Length 1210;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 506 CHALC 510

RESULT 52
US-09-715-249-2
; Sequence 2, Application US/09715249
; Patent No. 6790614
; GENERAL INFORMATION:
; APPLICANT: NOVARTIS AG
; APPLICANT: VERES, GABOR
; APPLICANT: PIPPIG, SUSANNE
; TITLE OF INVENTION: selectable cell surface marker genes
; FILE REFERENCE: 4-31192
; CURRENT APPLICATION NUMBER: US/09/715,249
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: us 60/166594
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: us 09/539248
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1210
; TYPE: PRT
; ORGANISM: EGFR
; US-09-715-249-2

Query Match 91.2%; Score 31; DB 4; Length 1210;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 506 CHALC 510

RESULT 53
US-08-893-534A-9
; Sequence 9, Application US/08893534A
; Patent No. 6031072
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: CELL ADHESION
; NUMBER OF SEQUENCES: 47
```

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/996,679  
; FILING DATE: 23-DEC-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 100086.401  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; MOLECULE TYPE: peptide  
US-08-996-679-9

Query Match 88.2%; Score 30; DB 3; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5  
DB 1 CHGVC 5

RESULT 54  
US-08-996-679-9  
; Sequence 9, Application US/08996679  
; Patent No. 6163071  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; TITLE OF INVENTION: CELL ADHESION  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/996,679  
; FILING DATE: 23-DEC-1997  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 100086.401C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: circular  
; MOLECULE TYPE: peptide  
US-08-996-679-9

Query Match 88.2%; Score 30; DB 3; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5  
DB 1 CHGVC 5

RESULT 55  
US-09-115-395-20  
; Sequence 20, Application US/09115395A  
; Patent No. 6207639  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NEURITE OUTGROWTH  
; FILE REFERENCE: 100086.401C3  
; CURRENT APPLICATION NUMBER: US/09/115.395A  
; CURRENT FILING DATE: 1998-07-14  
; EARLIER APPLICATION NUMBER: 08/996,679  
; EARLIER FILING DATE: 1997-12-23  
; EARLIER APPLICATION NUMBER: 08/893,534  
; EARLIER FILING DATE: 1997-07-11  
; EARLIER APPLICATION NUMBER: 60/021,612  
; EARLIER FILING DATE: 1996-07-12  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase  
; OTHER INFORMATION: Synthesis  
US-09-115-395-20

Query Match 88.2%; Score 30; DB 3; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5  
DB 1 CHGVC 5

RESULT 56  
US-09-507-102-9  
; Sequence 9, Application US/09507102  
; Patent No. 6326352  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED IP LAW GROUP PLLC  
; STREET: 6300 Bank of America Bldg., 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/507,102  
FILING DATE: 17-Feb-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/893,534  
FILING DATE: 11-JUL-1997  
APPLICATION NUMBER: US 60/021,612  
FILING DATE: 12-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Christiansen, William T.  
REGISTRATION NUMBER: 44,614  
REFERENCE/DOCKET NUMBER: 100086.401C10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
SEQUENCE CHARACTERISTICS:  
INFORMATION FOR SEQ ID NO: 9:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: circular  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-507-102-9

Query Match 88.2%; Score 30; DB 3; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||  
Db 1 CHGVC 5

RESULT 57  
US-09-250-059-11  
; Sequence 11, Application US/09250059  
; Patent No. 6333307  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NEURITE OUTGROWTH  
; FILE REFERENCE: 100086.401C6  
; CURRENT APPLICATION NUMBER: US/09/250,059  
; CURRENT FILING DATE: 1999-02-12  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic  
; OTHER INFORMATION: control peptide  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-09-250-059-11

Query Match 88.2%; Score 30; DB 3; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||

Db 1 CHGVC 5  
RESULT 58  
US-09-248-074-11  
; Sequence 11, Application US/09248074  
; Patent No. 6346512  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401C5  
; CURRENT APPLICATION NUMBER: US/09/248,074  
; CURRENT FILING DATE: 1999-02-10  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic  
; OTHER INFORMATION: control peptide  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-09-248-074-11

Query Match 88.2%; Score 30; DB 3; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||  
Db 1 CHGVC 5

RESULT 59  
US-09-357-717-11  
; Sequence 11, Application US/09357717  
; Patent No. 6417325  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR CANCER THERAPY  
; FILE REFERENCE: 100086.401C7  
; CURRENT APPLICATION NUMBER: US/09/357,717  
; CURRENT FILING DATE: 1999-07-20  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic  
; OTHER INFORMATION: control peptide  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-09-357-717-11

Query Match 88.2%; Score 30; DB 4; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||

Db 1 CHGVC 5

## RESULT 60

US-09-458-870-11  
; Sequence 11, Application US/09458870  
; Patent No. 6465427  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Anmar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401C8  
; CURRENT APPLICATION NUMBER: US/09/458,870  
; CURRENT FILING DATE: 1999-12-10  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic  
; OTHER INFORMATION: control peptide  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-09-458-870-11

Query Match 88.2%; Score 30; DB 4; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5  
DB 1 CHGVC 5

## RESULT 61

US-09-248-015-20  
; Sequence 20, Application US/09248015  
; Patent No. 6562786  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING APOPTOSIS  
; FILE REFERENCE: 100086.401C4  
; CURRENT APPLICATION NUMBER: US/09/248,015  
; CURRENT FILING DATE: 1999-02-10  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic  
; OTHER INFORMATION: control peptide  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-09-248-015-20

Query Match 88.2%; Score 30; DB 4; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5

Db 1 CHGVC 5

## RESULT 62

US-09-544-782-11  
; Sequence 11, Application US/09544782  
; Patent No. 6610821  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Anmar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401C9  
; CURRENT APPLICATION NUMBER: US/09/544,782  
; CURRENT FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic  
; OTHER INFORMATION: control peptide  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-09-544-782-11

Query Match 88.2%; Score 30; DB 4; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5  
DB 1 CHGVC 5

## RESULT 63

US-10-058-821-11  
; Sequence 11, Application US/10058821  
; Patent No. 6780845  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR CANCER THERAPY  
; FILE REFERENCE: 100086.401C12  
; CURRENT APPLICATION NUMBER: US/10/058,821  
; CURRENT FILING DATE: 2002-01-29  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic  
; OTHER INFORMATION: control peptide  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-10-058-821-11

Query Match 88.2%; Score 30; DB 4; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5

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Db          1 CHGVC 5
|||
; TITLE OF INVENTION: Mu-Conopeptides
; FILE REFERENCE: 2314-242
; CURRENT APPLICATION NUMBER: US/09/910,009A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,619
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/245,157
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/264,319
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: US 60/277,270
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 454
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Conus aulicus
; US-09-910-009A-454

Query Match      88.2%; Score 30; DB 4; Length 16;
Best Local Similarity 60.0%; Pred. No. 43;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      7 CHSIC 11

RESULT 64
US-09-910-009A-358
; Sequence 358, Application US/09910009A
; Patent No. 6727226
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; APPLICANT: Shen, Greg S.
; APPLICANT: Wagstaff, John D.
; TITLE OF INVENTION: Mu-Conopeptides
; FILE REFERENCE: 2314-242
; CURRENT APPLICATION NUMBER: US/09/910,009A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,619
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/245,157
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/264,319
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: US 60/277,270
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 358
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Conus aulicus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(16)
; OTHER INFORMATION: Xaa at residue 5 and 6 is Pro or Hyp
US-09-910-009A-358

Query Match      88.2%; Score 30; DB 4; Length 16;
Best Local Similarity 60.0%; Pred. No. 43;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      7 CHSIC 11

RESULT 65
US-09-910-009A-454
; Sequence 454, Application US/09910009A
; Patent No. 6727226
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; APPLICANT: Shen, Greg S.
; APPLICANT: Wagstaff, John D.
```

; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-331-625A-35

Query Match 88.2%; Score 30; DB 3; Length 17;  
Best Local Similarity 60.0%; Pred. No. 46;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
Db 8 CHSIC 12

## RESULT 67

US-09-494-151-35  
; Sequence 35, Application US/09494151  
; Patent No. 6372224  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Timothy J.  
; Klepfer, Sharon  
; Reed, Albert Paul  
; Jones, Elaine V.  
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses  
; Therefor  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation - Corporate  
; Patents  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/494,151  
; FILING DATE: 28-Jan-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/331,625  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 07/698,927  
; FILING DATE: 13-MAY-1991  
; APPLICATION NUMBER: US 07/613,066  
; FILING DATE: 14-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schreck, Patricia A.  
; REGISTRATION NUMBER: 33,777  
; REFERENCE/DOCKET NUMBER: SBC H85010-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5015  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
US-09-494-151-35

Query Match 88.2%; Score 30; DB 3; Length 17;  
Best Local Similarity 60.0%; Pred. No. 46;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
Db 8 CHSIC 12

## RESULT 68

US-09-972-484-35  
; Sequence 35, Application US/09972484  
; Patent No. 6602504  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Timothy J.  
; Klepfer, Sharon  
; Reed, Albert Paul  
; Jones, Elaine V.  
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses  
; Therefor  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation - Corporate  
; Patents  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/972,484  
; FILING DATE: 05-Oct-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/494,151  
; FILING DATE: 28-Jan-2000  
; APPLICATION NUMBER: 08/331,625  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 07/698,927  
; FILING DATE: 13-MAY-1991  
; APPLICATION NUMBER: US 07/613,066  
; FILING DATE: 14-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schreck, Patricia A.  
; REGISTRATION NUMBER: 33,777  
; REFERENCE/DOCKET NUMBER: SBC H85010-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5015  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
US-09-972-484-35

Query Match 88.2%; Score 30; DB 4; Length 17;  
Best Local Similarity 60.0%; Pred. No. 46;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
Db 8 CHSIC 12

## RESULT 69

US-09-910-009A-357  
; Sequence 357, Application US/09910009A  
; Patent No. 6727226

; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Garrett, James E.  
; APPLICANT: Watkins, Maren  
; APPLICANT: Cruz, Lourdes J.  
; APPLICANT: Shon, Ki-Joon  
; APPLICANT: Jacobsen, Richard  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Cartier, G. Edward  
; APPLICANT: Shen, Greg S.  
; APPLICANT: Wagstaff, John D.  
; TITLE OF INVENTION: Mu-Conopeptides  
; FILE REFERENCE: 2314-242  
; CURRENT APPLICATION NUMBER: US/09/910,009A  
; CURRENT FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: US 60/219,619  
; PRIOR FILING DATE: 2000-07-21  
; PRIOR APPLICATION NUMBER: US 60/245,157  
; PRIOR FILING DATE: 2000-11-03  
; PRIOR APPLICATION NUMBER: US 60/264,319  
; PRIOR FILING DATE: 2001-01-29  
; PRIOR APPLICATION NUMBER: US 60/277,270  
; PRIOR FILING DATE: 2001-03-21  
; NUMBER OF SEQ ID NOS: 520  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 357  
; LENGTH: 65  
; TYPE: PRT  
; ORGANISM: Conus aulicus  
US-09-910-009A-357

Query Match 88.2%; Score 30; DB 4; Length 65;  
Best Local Similarity 60.0%; Pred. No. 1.5e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
||:|  
Db 55 CHSIC 59

RESULT 70  
US-09-328-352-7139  
; Sequence 7139, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 7139  
; LENGTH: 145  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-7139

Query Match 88.2%; Score 30; DB 4; Length 145;  
Best Local Similarity 60.0%; Pred. No. 3e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
||:|  
Db 13 CHSIC 17

RESULT 71  
US-09-270-767-39899  
; Sequence 39899, Application US/09270767

; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 39899  
; LENGTH: 165  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-39899

Query Match 88.2%; Score 30; DB 4; Length 165;  
Best Local Similarity 80.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
||:|  
Db 107 CHVC 111

RESULT 72  
US-09-270-767-55116  
; Sequence 55116, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 55116  
; LENGTH: 165  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-55116

Query Match 88.2%; Score 30; DB 4; Length 165;  
Best Local Similarity 80.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
||:|  
Db 107 CHVC 111

RESULT 73  
US-08-331-625A-11  
; Sequence 11, Application US/08331625A  
; Patent No. 6057436  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Timothy J.  
; APPLICANT: Klepfer, Sharon  
; APPLICANT: Reed, Albert Paul  
; APPLICANT: Jones, Elaine V.  
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation - Corporate  
; ADDRESSEE: Patents  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA

```
;
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,625A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/880,194
; FILING DATE: 08-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: SBC H85010-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 203 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-331-625A-11
;
; Query Match 88.2%; Score 30; DB 3; Length 203;
; Best Local Similarity 60.0%; Pred. No. 4e+02;
; Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 CHAVC 5
; DB 182 CHSIC 186
;
; RESULT 74
; US-09-494-151-11
; Sequence 11, Application US/09494151
; Patent No. 6372224
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; Kieffer, Sharon
; Reed, Albert Paul
; Jones, Elaine V.
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
; THEREFOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; Patents
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/494,151
; FILING DATE: 28-Jan-2000
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/494,151
; FILING DATE: 28-Jan-2000
; APPLICATION NUMBER: 08/331,625
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; CLASSIFICATION: <Unknown>
```

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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/331,625
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: SBC H85010-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 203 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
; US-09-494-151-11
;
; Query Match 88.2%; Score 30; DB 3; Length 203;
; Best Local Similarity 60.0%; Pred. No. 4e+02;
; Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 CHAVC 5
; DB 182 CHSIC 186
;
; RESULT 75
; US-09-972-484-11
; Sequence 11, Application US/09972484
; Patent No. 6602504
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; Kieffer, Sharon
; Reed, Albert Paul
; Jones, Elaine V.
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
; THEREFOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; Patents
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,484
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/494,151
; FILING DATE: 28-Jan-2000
; APPLICATION NUMBER: 08/331,625
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
```



REFERENCE/DOCKET NUMBER: SBC H85010-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5015  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 203 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-972-484-11

Query Match 88.2%; Score 30; DB 4; Length 203;  
Best Local Similarity 60.0%; Pred. No. 4e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||  
Db 182 CHSIC 186

RESULT 76  
US-09-902-540-15175  
; Sequence 15175, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 15175  
; LENGTH: 234  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-15175

Query Match 88.2%; Score 30; DB 4; Length 234;  
Best Local Similarity 80.0%; Pred. No. 4.5e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||  
Db 215 CHATC 219

RESULT 77  
US-09-489-039A-9117  
; Sequence 9117, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 9117  
; LENGTH: 301  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-9117

Query Match 88.2%; Score 30; DB 4; Length 301;  
Best Local Similarity 80.0%; Pred. No. 5.6e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||  
Db 36 CHAAC 40

RESULT 78  
US-09-244-805-62  
; Sequence 62, Application US/09244805  
; Patent No. 6699660  
; GENERAL INFORMATION:  
; APPLICANT: Worley, Paul F.  
; APPLICANT: Lanahan, Anthony  
; APPLICANT: Goetz, Bernard  
; APPLICANT: Heimisch, Holger  
; APPLICANT: Kuner, Rohini  
; APPLICANT: Scheek, Sigrid  
; APPLICANT: Nikolich, Karoly  
; APPLICANT: Zhukovski, Eugene  
; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 10496/004001  
; CURRENT APPLICATION NUMBER: US/09/244,805  
; CURRENT FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: 60/074,518  
; PRIOR FILING DATE: 1998-02-12  
; PRIOR APPLICATION NUMBER: 60/074,135  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 62  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-244-805-62

Query Match 88.2%; Score 30; DB 4; Length 342;  
Best Local Similarity 80.0%; Pred. No. 6.3e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||  
Db 141 CHVC 145

RESULT 79  
US-07-857-224B-85  
; Sequence 85, Application US/07857224B  
; Patent No. 5958784  
; GENERAL INFORMATION:  
; APPLICANT: Benner, Steven A.  
; TITLE OF INVENTION: Predicting Folded Structures of Proteins  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Steven A. Benner  
; STREET: Hadlaubstrasse 151  
; CITY: Zurich  
; STATE: none  
; COUNTRY: Switzerland  
; ZIP: (note: this is an international post code) CH-8092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 7.0  
; SOFTWARE: Microsoft Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/857,224B  
; FILING DATE: 03/25/92  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA: none

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (International) 41 1 632 2830
; TELEFAX: (International) 41 1 262 2437
; TELEX: none
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; ORIGINAL SOURCE:
; ORGANISM: mouse
; FEATURE: Alcohol dehydrogenase, Table 3 Column 6
; PUBLICATION INFORMATION:
; AUTHORS:
; AUTHORS: Joernvall, H.
; AUTHORS: Persson, M.
; AUTHORS: Jeffery, J.
; TITLE: Alcohol dehydrogenases
; JOURNAL: Proceedings of the National Academy of Sciences, USA
; VOLUME: 78
; PAGES: 4226-4230
; DATE: 1981
; US-07-857-224B-85

Query Match      88.2%; Score 30; DB 2; Length 374;
Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      282 CHAAC 286

RESULT 80
US-09-902-540-10986
; Sequence 10986, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10986
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
; US-09-902-540-10986

Query Match      88.2%; Score 30; DB 4; Length 525;
Best Local Similarity 80.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      206 CHVVC 210

RESULT 81
US-09-270-767-44409
; Sequence 44409, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44409
; LENGTH: 777
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-44409

Query Match      88.2%; Score 30; DB 4; Length 777;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      215 CHAAC 219

RESULT 82
US-08-331-625A-52
; Sequence 52, Application US/08331625A
; Patent No. 6057436
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; APPLICANT: Klepfer, Sharon
; APPLICANT: Reed, Albert Paul
; APPLICANT: Jones, Elaine V.
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
; TITLE OF INVENTION: Therefor
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; ADDRESS: Patents
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,625A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/880,194
; FILING DATE: 08-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: SBC H85010-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1101 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
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US-08-331-625A-52

Query Match 88.2%; Score 30; DB 3; Length 1101;  
Best Local Similarity 60.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
DB 1080 CHSIC 1084

RESULT 83

US-09-494-151-52  
; Sequence 52, Application US/09494151  
; Patent No. 6372224  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Timothy J.  
; Klepfer, Sharon  
; Reed, Albert Paul  
; Jones, Elaine V.  
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses  
; Therefor  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation - Corporate  
; Patents  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/494,151  
; FILING DATE: 28-Jan-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/331,625  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 07/698,927  
; FILING DATE: 13-MAY-1991  
; APPLICATION NUMBER: US 07/613,066  
; FILING DATE: 14-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schreck, Patricia A.  
; REGISTRATION NUMBER: 33,777  
; REFERENCE/DOCKET NUMBER: SBC H85010-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5015  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1101 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Query Match 88.2%; Score 30; DB 3; Length 1101;  
Best Local Similarity 60.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
DB 1080 CHSIC 1084

RESULT 84

US-09-972-484-52

; Sequence 52, Application US/09972484  
; Patent No. 6602504  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Timothy J.  
; Klepfer, Sharon  
; Reed, Albert Paul  
; Jones, Elaine V.  
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses  
; Therefor  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation - Corporate  
; Patents  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/972,484  
; FILING DATE: 05-Oct-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/494,151  
; FILING DATE: 28-Jan-2000  
; APPLICATION NUMBER: 08/331,625  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 07/698,927  
; FILING DATE: 13-MAY-1991  
; APPLICATION NUMBER: US 07/613,066  
; FILING DATE: 14-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schreck, Patricia A.  
; REGISTRATION NUMBER: 33,777  
; REFERENCE/DOCKET NUMBER: SBC H85010-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5015  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1101 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Query Match 88.2%; Score 30; DB 4; Length 1101;  
Best Local Similarity 60.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
DB 1080 CHSIC 1084

RESULT 85

US-08-308-872B-2  
; Sequence 2, Application US/08308872B  
; Patent No. 5661006  
; GENERAL INFORMATION:  
; APPLICANT: BROWN, Thomas David Kay  
; APPLICANT: HORSBURGH, Brian Colin  
; TITLE OF INVENTION: CANINE CORONAVIRUS SUBUNIT VACCINE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Akzo No. 5661006el Patent Department

STREET: 1300 Piccard Drive, Suite 206  
CITY: Rockville  
STATE: Maryland  
COUNTRY: U.S.A.  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/308,872B  
FILING DATE: 19-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,846  
FILING DATE: 05-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/872,641  
FILING DATE: 24-APR-1992  
APPLICATION NUMBER: EP 91.303.737.0  
FILING DATE: 25-APR-1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Gormley, Mary E.  
REGISTRATION NUMBER: 34,409  
TELEPHONE: (301) 258-5200  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1443 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Canina corona virus  
STRAIN: CCV-6  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..1443  
OTHER INFORMATION: /label= CCV6\_Spike  
US-08-308-872B-2

Query Match 88.2%; Score 30; DB 1; Length 1443;  
Best Local Similarity 60.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
Db 1422 CHSIC 1426

RESULT 86  
US-08-308-872B-4  
Sequence 4, Application US/08308872B  
Patent No. 5661006  
GENERAL INFORMATION:  
APPLICANT: BROWN, Thomas David Kay  
APPLICANT: HORSBURGH, Brian Colin  
TITLE OF INVENTION: CANINE CORONAVIRUS SUBUNIT VACCINE  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Akzo No. 5661006el Patent Department  
STREET: 1300 Piccard Drive, Suite 206  
CITY: Rockville  
STATE: Maryland  
COUNTRY: U.S.A.  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/308,872B  
FILING DATE: 19-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,846  
FILING DATE: 05-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/872,641  
FILING DATE: 24-APR-1992  
APPLICATION NUMBER: EP 91.303.737.0  
FILING DATE: 25-APR-1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Gormley, Mary E.  
REGISTRATION NUMBER: 34,409  
TELEPHONE: (301) 258-5200  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1451 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Canine corona virus  
STRAIN: CCVinsAVC-1  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..1451  
OTHER INFORMATION: /label= CCVinsAVC-1\_Spike  
US-08-308-872B-4  
Query Match 88.2%; Score 30; DB 1; Length 1451;  
Best Local Similarity 60.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
Db 1430 CHSIC 1434

RESULT 87  
US-08-331-625A-2  
Sequence 2, Application US/08331625A  
Patent No. 6057436  
GENERAL INFORMATION:  
APPLICANT: Miller, Timothy J.  
APPLICANT: Klepfer, Sharon  
APPLICANT: Reed, Albert Paul  
APPLICANT: Jones, Elaine V.  
TITLE OF INVENTION: Canine Coronavirus S Gene and Uses  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation - Corporate  
ADDRESS: Patents  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-2799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331,625A  
FILING DATE:  
CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/880,194  
;; FILING DATE: 08-MAY-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/698,927  
;; FILING DATE: 13-MAY-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/613,066  
;; FILING DATE: 14-NOV-1990  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Schreck, Patricia A.  
;; REGISTRATION NUMBER: 33,777  
;; REFERENCE/DOCKET NUMBER: SBC H85010-1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (215) 270-5015  
;; TELEFAX: (215) 270-5090  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1452 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-331-625A-2

Query Match 88.2%; Score 30; DB 3; Length 1452;  
Best Local Similarity 60.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
Db 1431 CHSIC 1435

RESULT 88  
US-09-494-151-2  
; Sequence 2, Application US/09494151  
; Patent No. 6372224  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Timothy J.  
; Klepfer, Sharon  
; Reed, Albert Paul  
; Jones, Elaine V.  
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses  
; Therefor  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation - Corporate  
; Patents  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/494,151  
; FILING DATE: 28-Jan-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/331,625  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 07/698,927  
; FILING DATE: 13-MAY-1991  
; APPLICATION NUMBER: US 07/613,066  
; FILING DATE: 14-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schreck, Patricia A.  
; REGISTRATION NUMBER: 33,777  
; REFERENCE/DOCKET NUMBER: SBC H85010-1

;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (215) 270-5015  
;; TELEFAX: (215) 270-5090  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1452 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-494-151-2

Query Match 88.2%; Score 30; DB 3; Length 1452;  
Best Local Similarity 60.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
Db 1431 CHSIC 1435

RESULT 89  
US-09-972-484-2  
; Sequence 2, Application US/09972484  
; Patent No. 6602504  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Timothy J.  
; Klepfer, Sharon  
; Reed, Albert Paul  
; Jones, Elaine V.  
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses  
; Therefor  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation - Corporate  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/972,484  
; FILING DATE: 05-Oct-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/494,151  
; FILING DATE: 28-Jan-2000  
; APPLICATION NUMBER: 08/331,625  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 07/698,927  
; FILING DATE: 13-MAY-1991  
; APPLICATION NUMBER: US 07/613,066  
; FILING DATE: 14-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schreck, Patricia A.  
; REGISTRATION NUMBER: 33,777  
; REFERENCE/DOCKET NUMBER: SBC H85010-1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (215) 270-5015  
;; TELEFAX: (215) 270-5090  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1452 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-972-484-2

Query Match 88.2%; Score 30; DB 4; Length 1452;  
Best Local Similarity 60.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
DB 1431 CHSIC 1435

RESULT 90

PCT-US93-04384-18  
; Sequence 18, Application PC/TUS9304384  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Timothy J.  
; APPLICANT: Klepfer, Sharon  
; APPLICANT: Reed, Albert Paul  
; APPLICANT: Jones, Elaine V.  
; TITLE OF INVENTION: Compositions and Methods for Vaccination  
; TITLE OF INVENTION: Against Coronaviruses  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation - Corporate  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/04384  
; FILING DATE: 19930507  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/882,171  
; FILING DATE: 08-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/698,927  
; FILING DATE: 13-MAY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/613,066  
; FILING DATE: 14-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schreck, Patricia A.  
; REGISTRATION NUMBER: 33,777  
; REFERENCE/DOCKET NUMBER: SBC H85009-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5015  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1452 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US93-04384-18

Query Match 88.2%; Score 30; DB 5; Length 1452;  
Best Local Similarity 60.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
DB 1431 CHSIC 1435

RESULT 91

PCT-US93-04692-2

; Sequence 2, Application PC/TUS9304692  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Timothy J.  
; APPLICANT: Klepfer, Sharon  
; APPLICANT: Reed, Albert Paul  
; APPLICANT: Jones, Elaine V.  
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses  
; TITLE OF INVENTION: Therefor  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation - Corporate  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/04692  
; FILING DATE: 19930507  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/880,194  
; FILING DATE: 08-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/698,927  
; FILING DATE: 13-MAY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/613,066  
; FILING DATE: 14-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schreck, Patricia A.  
; REGISTRATION NUMBER: 33,777  
; REFERENCE/DOCKET NUMBER: SBC H85010-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5015  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1452 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US93-04692-2

Query Match 88.2%; Score 30; DB 5; Length 1452;  
Best Local Similarity 60.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
DB 1431 CHSIC 1435

RESULT 92

US-08-392-459-22  
; Sequence 22, Application US/08392459  
; Patent No. 6280974  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham, Corporation  
; TITLE OF INVENTION: Recombinant Feline Coronavirus S  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 54  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia

```
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,459
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T.
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: SBC 14532B
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1454 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-392-459-22

Query Match 88.2%; Score 30; DB 3; Length 1454;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 1433 CHSIC 1437

RESULT 93
; US-08-392-459-26
; Sequence 26, Application US/08392459
; Patent No. 6280974
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; TITLE OF INVENTION: Recombinant Feline Coronavirus S
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,459
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T.
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: SBC 14532B
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1454 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-392-459-22
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T.
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: SBC 14532B
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1454 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-392-459-26

Query Match 88.2%; Score 30; DB 3; Length 1454;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 1433 CHSIC 1437

RESULT 94
; US-09-854-799-22
; Sequence 22, Application US/09854799
; Patent No. 6642359
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; TITLE OF INVENTION: Recombinant Feline Coronavirus S
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/854,799
; FILING DATE: 14-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/392,459
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T.
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: SBC 14532B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1454 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
; US-09-854-799-22

Query Match 88.2%; Score 30; DB 4; Length 1454;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 CHAVC 5
Db      1433 CHSIC 1437

RESULT 95
US-09-854-799-26
; Sequence 26, Application US/09854799
; Patent No. 6642359
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; TITLE OF INVENTION: Recombinant Feline Coronavirus S
;   Proteins
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/854,799
; FILING DATE: 14-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/392,459
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T.
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: SBC 14532B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1454 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-854-799-26

Query Match      88.2%; Score 30; DB 4; Length 1454;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      1433 CHSIC 1437

RESULT 96
PCT-US91-08525-22
; Sequence 22, Application PC/TUS9108525
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; TITLE OF INVENTION: Recombinant Feline Coronavirus S
;   Proteins
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08525
; FILING DATE: 19911114
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; PRIOR APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T.
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: SBC 14532B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1454 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
PCT-US91-08525-22

Query Match      88.2%; Score 30; DB 5; Length 1454;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      1433 CHSIC 1437

RESULT 97
PCT-US91-08525-26
; Sequence 26, Application PC/TUS9108525
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; TITLE OF INVENTION: Recombinant Feline Coronavirus S
;   Proteins
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08525
; FILING DATE: 19911114
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; PRIOR APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T.
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: SBC 14532B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1454 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
PCT-US91-08525-22

Query Match      88.2%; Score 30; DB 5; Length 1454;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```



```
; NAME: King, William T.
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: SBC 14532B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1454 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-08525-26

Query Match      88.2%; Score 30; DB 5; Length 1454;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      1433 CHSIC 1437

RESULT 98
PCT-US93-04384-2
; Sequence 2, Application PC/TUS9304384
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; APPLICANT: Klepfer, Sharon
; APPLICANT: Reed, Albert Paul
; APPLICANT: Jones, Elaine V.
; TITLE OF INVENTION: Compositions and Methods for Vaccination
; TITLE OF INVENTION: Against Coronaviruses
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; ADDRESSEE: Patents
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/04384
; FILING DATE: 19930507
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/882,171
; FILING DATE: 08-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: SBC H85009-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1454 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-04384-8

Query Match      88.2%; Score 30; DB 5; Length 1454;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      1433 CHSIC 1437

RESULT 100
```

```
PCT-US93-04384-2

Query Match      88.2%; Score 30; DB 5; Length 1454;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      1433 CHSIC 1437

RESULT 99
PCT-US93-04384-8
; Sequence 8, Application PC/TUS9304384
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; APPLICANT: Klepfer, Sharon
; APPLICANT: Reed, Albert Paul
; APPLICANT: Jones, Elaine V.
; TITLE OF INVENTION: Compositions and Methods for Vaccination
; TITLE OF INVENTION: Against Coronaviruses
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; ADDRESSEE: Patents
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/04384
; FILING DATE: 19930507
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/882,171
; FILING DATE: 08-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: SBC H85009-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1454 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-04384-8

Query Match      88.2%; Score 30; DB 5; Length 1454;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      1433 CHSIC 1437

RESULT 100
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PCT-US93-04384-16  
; Sequence 16, Application PC/TUS9304384  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Timothy J.  
; APPLICANT: Klepfer, Sharon  
; APPLICANT: Reed, Albert Paul  
; APPLICANT: Jones, Elaine V.  
; TITLE OF INVENTION: Compositions and Methods for Vaccination  
; TITLE OF INVENTION: Against Coronaviruses  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation - Corporate  
; ADDRESSEE: Patents  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/04384  
; FILING DATE: 19930507  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/882,171  
; FILING DATE: 08-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/698,927  
; FILING DATE: 13-MAY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/613,066  
; FILING DATE: 14-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schreck, Patricia A.  
; REGISTRATION NUMBER: 33,777  
; REFERENCE/DOCKET NUMBER: SBC H85009-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5015  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1454 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US93-04384-16

Query Match 88.2%; Score 30; DB 5; Length 1454;  
Best Local Similarity 60.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
Db 1433 CHSIC 1437

Search completed: July 27, 2005, 00:02:32  
Job time : 42 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 26, 2005, 23:51:45 ; Search time 39 Seconds  
(without alignments)  
12.335 Million cell updates/sec

Title: US-10-632-678-10

Perfect score: 34

Sequence: 1 CHAVC 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	244	2	hypothetical prote
2	33	97.1	402	1	nonstructural prote
3	33	97.1	402	1	hypothetical prote
4	33	97.1	428	2	hypothetical prote
5	33	97.1	668	1	noncapsid protein
6	33	97.1	672	1	noncapsid protein
7	33	97.1	672	1	noncapsid protein
8	33	97.1	721	1	noncapsid protein
9	31	91.2	171	2	hypothetical prote
10	31	91.2	171	2	hypothetical prote
11	31	91.2	243	2	osmotin - common t
12	31	91.2	251	2	protein F21J9.10 [
13	31	91.2	307	1	thymidylate synth
14	31	91.2	307	2	thymidylate synth
15	31	91.2	313	1	thymidylate synth
16	31	91.2	373	2	hypothetical prote
17	31	91.2	563	2	succinate dehydrog
18	31	91.2	630	2	protein C43E11.8 [
19	31	91.2	1111	2	hypothetical prote
20	31	91.2	1210	1	epidermal growth f
21	31	91.2	2195	2	hypothetical prote
22	30	88.2	67	2	hypothetical prote
23	30	88.2	106	2	hypothetical prote
24	30	88.2	108	2	hypothetical prote
25	30	88.2	122	2	hypothetical prote
26	30	88.2	154	2	hypothetical prote
27	30	88.2	163	2	hypothetical prote
28	30	88.2	179	2	hypothetical prote
29	30	88.2	184	1	interferon alpha-I

30	88.2	319	2	T34728	hypothetical prote
31	88.2	372	2	F70467	hypothetical prote
32	88.2	375	1	DEMSAA	alcohol dehydrogen
33	88.2	433	2	A39556	triacylglycerol li
34	88.2	523	2	S64826	probable membrane
35	88.2	760	2	F86281	protein F10B6.14 [
36	88.2	769	2	S55554	male-specific leth
37	88.2	843	2	A27131	epidermal growth f
38	88.2	1436	2	B81704	conserved hypothet
39	88.2	1447	1	VG1HE3	E2 glycoprotein pr
40	88.2	1447	1	VG1HE2	E2 glycoprotein pr
41	88.2	1449	1	A43573	E2 glycoprotein pr
42	88.2	1449	1	VG1HFS	E2 glycoprotein pr
43	88.2	1449	2	S47423	E2 glycoprotein pr
44	88.2	1451	1	JQ1719	E2 glycoprotein pr
45	88.2	1452	1	VG1H79	E2 glycoprotein pr
46	88.2	1453	2	S41453	spike protein - ca
47	88.2	1766	2	A42125	trophozoite cystei
48	85.3	67	2	B96981	hypothetical prote
49	85.3	120	2	T27516	hypothetical prote
50	85.3	187	1	QOEC30	prepilin peptidase
51	85.3	187	2	D85934	prepilin peptidase
52	85.3	187	2	B98089	prepilin peptidase
53	85.3	219	2	G71343	hypothetical prote
54	85.3	228	2	A82147	ABC transporter, A
55	85.3	234	2	F76342	hypothetical prote
56	85.3	261	2	F72426	iron-sulfur cluste
57	85.3	265	2	T17632	hypothetical prote
58	85.3	307	2	T52387	hypothetical prote
59	85.3	330	2	I40700	type II site-spaci
60	85.3	336	2	A64378	hypothetical prote
61	85.3	337	2	C64434	hypothetical prote
62	85.3	343	2	A64513	hypothetical prote
63	85.3	359	2	E64425	hypothetical prote
64	85.3	380	2	H87344	esterase, probable
65	85.3	416	2	F83010	probable oxidoredu
66	85.3	418	2	AC0809	xanthosine permeas
67	85.3	418	2	E65014	xanthosine permeas
68	85.3	440	2	T52320	10-deacetylacat
69	85.3	461	2	T00918	hypothetical prote
70	85.3	590	2	T20537	hypothetical prote
71	85.3	696	2	JC7351	foliitropin recept
72	85.3	710	2	T20635	hypothetical prote
73	85.3	767	2	T39715	probable transcrip
74	85.3	946	2	D96503	protein F9C16.9 [1
75	85.3	1339	2	JC4387	epidermal growth f
76	85.3	1342	2	A36223	kinase-related tra
77	85.3	1737	2	T00209	MEGF8 protein - hu
78	85.3	2269	2	T18472	hypothetical prote
79	82.4	110	2	T38057	hypothetical prote
80	82.4	131	2	T17545	hypothetical prote
81	82.4	157	2	T23781	hypothetical prote
82	82.4	157	2	T46204	interferon-alpha -
83	82.4	187	2	I46206	interferon-alpha -
84	82.4	227	2	AC0359	probable membrane
85	82.4	230	2	T43487	hypothetical prote
86	82.4	239	1	C44954	hypothetical prote
87	82.4	260	2	D86266	hypothetical prote
88	82.4	290	2	AG0041	L-rhamnose operon
89	82.4	295	2	J50174	frizzled protein-2
90	82.4	308	2	T22393	hypothetical prote
91	82.4	351	2	JC7096	leukotriene B4 rec
92	82.4	358	2	T38429	connexin40 - human
93	82.4	375	1	A49107	alcohol dehydrogen
94	82.4	403	2	S07825	hypothetical prote
95	82.4	407	2	S44909	ZK686.4 protein -
96	82.4	418	2	B36067	thyroid hormone re
97	82.4	424	2	A55089	vasopressin V3 rec
98	82.4	436	2	T03152	transcription cont
99	82.4	455	1	JQ0507	adenosylmethionine
100	82.4	460	2	S58882	protein kinase Cds

## ALIGNMENTS

## RESULT 1

E84885  
hypothetical protein At2g45010 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: E84885  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: E84885  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-244 <STO>  
A:Cross-references: UNIPROT:Q8L3T0; GB:AE002093; NID:g4895249; PIDN:AAD32834.1; GSPDB:GN  
C:Genetics:  
A:Gene: At2g45010  
A:Map position: 2

Query Match 100.0%; Score 34; DB 2; Length 244;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
|||:  
Db 106 CHAVC 110

## RESULT 2

MNXRPC  
nonstructural protein NS34 - porcine rotavirus C (strain Cowden)  
C:Species: porcine rotavirus C  
C>Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
C:Accession: A41040  
R:Qian, Y.; Jiang, B.; Saif, L.J.; Kang, S.Y.; Ojeh, C.K.; Green, K.Y.  
Virology 184, 752-757, 1991  
A:Title: Molecular analysis of the gene 6 from a porcine group C rotavirus that encodes  
A:Reference number: A41040; MUID:91361567; PMID:1653496  
A:Accession: A41040  
A:Molecule type: genomic RNA  
A:Residues: 1-402 <QIA>  
A:Cross-references: UNIPROT:P27586; GB:M69115; NID:g333307; PIDN:AAA47087.1; PID:g333308  
C:Genetics:  
A:Map position: segment 6  
C:Superfamily: rotavirus nonstructural protein  
C:Keywords: nonstructural protein

Query Match 97.1%; Score 33; DB 1; Length 402;  
Best Local Similarity 80.0%; Pred. No. 92;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
|||:  
Db 280 CHAIC 284

## RESULT 3

S35639  
hypothetical protein - bovine rotavirus C  
C:Species: bovine rotavirus C  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S35639  
R:Jiang, B.; Tsunemitsu, H.; Gentsch, J.R.; Saif, L.J.; Glass, R.I.  
Nucleic Acids Res. 21, 2250, 1993  
A:Title: Nucleotide sequences of genes 6 and 10 of a bovine group C rotavirus.  
A:Reference number: S35639; MUID:93275758; PMID:8389040  
A:Accession: S35639  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-402 <JIA>

A:Cross-references: UNIPROT:P34717; EMBL:L12390

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1993  
C:Superfamily: rotavirus nonstructural protein

Query Match 97.1%; Score 33; DB 2; Length 402;  
Best Local Similarity 80.0%; Pred. No. 92;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
|||:  
Db 280 CHAIC 284

## RESULT 4

T48008  
hypothetical protein T17J13.120 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C:Accession: T48008  
R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer, I.  
submitted to the Protein Sequence Database, February 2000  
A:Reference number: Z24482  
A:Accession: T48008  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-428 <RIE>

A:Cross-references: UNIPROT:Q9MIQ8; EMBL:AL138651  
A:Experimental source: cultivar Columbia; BAC clone T17J13  
C:Genetics:  
A:Map position: 3  
A:Introns: 137/3  
A>Note: T17J13.120

Query Match 97.1%; Score 33; DB 2; Length 428;  
Best Local Similarity 80.0%; Pred. No. 96;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
|||:  
Db 153 CHAIC 157

## RESULT 5

A4276  
noncapsid protein NS1 - parvovirus LuIII  
C:Species: parvovirus LuIII  
C>Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004  
R:Difffoot, N.; Chen, K.C.; Bates, R.C.; Lederma, M.  
Virology 192, 339-345, 1993  
A:Title: The complete nucleotide sequence of parvovirus LuIII and localization of a unique  
A:Reference number: A44276; MUID:93297126; PMID:8517025  
A:Accession: A44276  
A>Status: translation not shown

QY 1 CHAVC 5  
|||:  
Db 378 CHAIC 382

## RESULT 6

UYPVIM

noncapsid protein NS1 - minute virus of mice  
 C;Species: minute virus of mice, murine parvovirus  
 C;Date: 14-Nov-1983 #sequence\_revision 28-Aug-1985 #text\_change 09-Jul-2004  
 C;Accession: A03696  
 R;Astell, C.R.; Thomson, M.; Merchlinsky, M.; Ward, D.C.  
 Nucleic Acids Res. 11, 999-1018, 1983  
 A;Title: The complete DNA sequence of minute virus of mice, an autonomous parvovirus.  
 A;Reference number: A03696; MUID:83143341; PMID:6298737  
 A;Accession: A03696  
 A;Molecule type: DNA  
 A;Residues: 1-672 <AST>  
 A;Cross-references: UNIPROT:P03134; EMBL:V01115  
 C;Superfamily: parvovirus noncapsid protein  
 C;Keywords: noncapsid protein

Query Match 97.1%; Score 33; DB 1; Length 672;  
 Best Local Similarity 80.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 |||||  
 Db 378 CHAIC 382

RESULT 7  
 UVPV1  
 noncapsid protein NS1 - parvovirus H1  
 C;Species: parvovirus H1  
 A;Note: host Homo sapiens (man)  
 C;Date: 14-Nov-1983 #sequence\_revision 14-Nov-1983 #text\_change 09-Jul-2004  
 C;Accession: A03695  
 R;Rhode III, S.L.; Paradiso, P.R.  
 J. Virol. 45, 173-184, 1983  
 A;Title: Parvovirus genome: nucleotide sequence of H-1 and mapping of its genes by hybridization  
 A;Reference number: A03695; MUID:83112183; PMID:6823009  
 A;Accession: A03695  
 A;Molecule type: DNA  
 A;Residues: 1-672 <RHO>  
 A;Cross-references: UNIPROT:P03133; EMBL:X01457; NID:g60993; PIDN:CAA25689.1; PID:g60994  
 C;Superfamily: parvovirus noncapsid protein  
 C;Keywords: noncapsid protein

Query Match 97.1%; Score 33; DB 1; Length 672;  
 Best Local Similarity 80.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 |||||  
 Db 378 CHAIC 382

RESULT 8  
 UVPV1M  
 noncapsid protein NS1 - minute virus of mice (strain MMV1)  
 C;Species: minute virus of mice, murine parvovirus  
 C;Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 09-Jul-2004  
 C;Accession: A23510  
 R;Sahli, R.; McMaster, G.K.; Hirt, B.  
 Nucleic Acids Res. 13, 3617-3633, 1985  
 A;Title: DNA sequence comparison between two tissue-specific variants of the autonomous  
 A;Reference number: A23008; MUID:85242059; PMID:3855242  
 A;Accession: A23008  
 A;Molecule type: DNA  
 A;Residues: 1-721 <SAH>  
 A;Cross-references: UNIPROT:Q84363; EMBL:X02481  
 R;Astell, C.R.; Gardiner, E.M.; Tattersall, P.  
 J. Virol. 57, 656-669, 1986  
 A;Title: DNA sequence of the lymphotropic variant of minute virus of mice, MMV(i), and  
 A;Reference number: A29510; MUID:86115415; PMID:3502703  
 A;Accession: A29510  
 A;Molecule type: DNA  
 A;Residues: 1-645, 'I', 647-721 <AST>  
 A;Cross-references: EMBL:M12032; NID:g332289; PIDN:AAA69566.1; PID:g825477

C;Superfamily: parvovirus noncapsid protein  
 C;Keywords: noncapsid protein

Query Match 97.1%; Score 33; DB 1; Length 721;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 |||||  
 Db 427 CHAIC 431

# RESULT 9

S09903  
 hypothetical protein IRL10 precursor - human cytomegalovirus (strain AD169)  
 C;Species: human cytomegalovirus, human herpesvirus 5  
 A;Note: host Homo sapiens (man)  
 C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
 C;Accession: S09903  
 R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.;  
 M.; Barrell, B.G.  
 Curr. Top. Microbiol. Immunol. 154, 125-169, 1990

A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus  
 A;Reference number: S09749; MUID:90269039; PMID:2161319  
 A;Accession: S09903  
 A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA  
 A;Residues: 1-171 <CHE>  
 A;Cross-references: UNIPROT:P16808; EMBL:X17403; NID:g59591; PIDN:CAA35300.1; PID:g17809  
 A;Note: this sequence was submitted to the EMBL Data Library, December 1989

C;Keywords: glycoprotein; transmembrane protein  
 F;1-25/Domain: signal sequence #status predicted <SIG>  
 F;26-171/Product: hypothetical protein IRL10 #status predicted <MAT>  
 F;70-103/Domain: transmembrane #status predicted <TMW>  
 F;48,49,56,108/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.2%; Score 31; DB 2; Length 171;  
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 |||||  
 Db 60 CHAMC 64

# RESULT 10

S09759  
 hypothetical protein TRL10 precursor - human cytomegalovirus (strain AD169)  
 C;Species: human cytomegalovirus, human herpesvirus 5  
 A;Note: host Homo sapiens (man)  
 C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
 C;Accession: S09759  
 R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.;  
 M.; Barrell, B.G.  
 Curr. Top. Microbiol. Immunol. 154, 125-169, 1990

A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus  
 A;Reference number: S09749; MUID:90269039; PMID:2161319  
 A;Accession: S09759  
 A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA  
 A;Residues: 1-171 <CHE>  
 A;Cross-references: UNIPROT:Q69029; EMBL:X17403; NID:g59591; PIDN:CAA35458.1; PID:g59601

A;Note: this sequence was submitted to the EMBL Data Library, December 1989  
 C;Keywords: glycoprotein; transmembrane protein  
 F;1-25/Domain: signal sequence #status predicted <SIG>  
 F;26-171/Product: hypothetical protein TRL10 #status predicted <MAT>  
 F;70-103/Domain: transmembrane #status predicted <TMW>  
 F;48,49,56,108/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.2%; Score 31; DB 2; Length 171;  
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



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Db      189 CHALC 193

RESULT 15
YXHU7
thymidylate synthase (EC 2.1.1.45) - human
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 16-Aug-2004
C/Accession: A23047; J00120; A22393; A33842
R/Takeishi, K.; Kaneda, S.; Ayusawa, D.; Shimizu, K.; Gotoh, O.; Seno, T.
Nucleic Acids Res. 13, 2035-2043, 1985
A/Title: Nucleotide sequence of a functional cDNA for human thymidylate synthase.
A/Reference number: A23047; MUID:85215597; PMID:2987839
A/Accession: A23047
A/Molecule type: mRNA
A/Residues: 1-313 <TAK>
A/Cross-references: UNIPROT:P04818; EMBL:X02308; NID:g37478; PIDN:CAA26178.1; PID:g37479
R/Kaneda, S.; Nalbantoglu, J.; Takeishi, K.; Shimizu, K.; Gotoh, O.; Seno, T.; Ayusawa,
J. Biol. Chem. 265, 20277-20284, 1990
A/Title: Structural and Functional Analysis of the Human Thymidylate Synthase Gene.
A/Reference number: 155318; MUID:91056070; PMID:2243092
A/Accession: 155318
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-313 <RES>
A/Cross-references: GB:D00596; NID:g220135; PIDN:BAA00472.1; PID:g220136
R/Takeishi, K.; Kaneda, S.; Ayusawa, D.; Shimizu, K.; Gotoh, O.; Seno, T.
J. Biochem. 106, 575-583, 1989
A/Title: Human thymidylate synthase gene: isolation of phage clones which cover a function
A/Reference number: J00120; MUID:90110051; PMID:2532645
A/Accession: J00120
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-68 <TA2>
A/Cross-references: GB:D00517; NID:g220133; PIDN:BAA00404.1; PID:g2160415
R/Shimizu, K.; Ayusawa, D.; Takeishi, K.; Seno, T.
J. Biochem. 97, 845-850, 1995
A/Title: Purification and NH2-terminal amino acid sequence of human thymidylate synthase
A/Reference number: A22393; MUID:85261174; PMID:3839505
A/Accession: A22393
A/Molecule type: protein
A/Residues: 2-25 <SHI>
R/Davissou, V.J.; Sirawaraporn, W.; Santi, D.V.
J. Biol. Chem. 264, 9145-9148, 1989
A/Title: Expression of human thymidylate synthase in Escherichia coli.
A/Reference number: A33842; MUID:89255401; PMID:2655695
A/Accession: A33842
A/Molecule type: protein
A/Residues: 2-10 <DAV>
C/Genetics:
A/Gene: GDB:TYMS
A/Cross-references: GDB:120465; OMIM:188350
A/Map position: 18p11.32-18p11.32
A/Introns: 69/1; 93/3; 152/1; 186/1; 244/3; 268/3
C/Superfamily: Thymidylate synthase; thymidylate synthase homology
C/Keywords: deoxyribonucleotide biosynthesis; methyltransferase
F:30-313/Domain: thymidylate synthase homology <TDS>
F:199/Active site: Cys #status predicted

Query Match      91.2%; Score 31; DB 1; Length 313;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      195 CHALC 199

RESULT 16
T25920
hypothetical protein T27A3.7 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans

Query Match      91.2%; Score 31; DB 2; Length 563;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      41 CHSVC 45

RESULT 18
G87753
protein C43E11.8 [imported] - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G87753
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A/Reference number: A75000; MUID:99069613; PMID:9851916
A/Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A/Accession: G87753

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C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T25920
R/Murray, J.; Wohldmann, P.
submitted to the EMBL Data Library, February 1997
A/Description: The sequence of C. elegans cosmid T27A3.
A/Reference number: 220110
A/Accession: T25920
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-373 <MUR>
A/Cross-references: UNIPROT:P91501; EMBL:U88180; PIDN:AAB42300.1; GSPDB:GN00019; CESP:T2
A/Experimental source: strain Bristol N2; clone T27A3
C/Genetics:
A/Gene: CESP:T27A3.7
A/Map position: 1
A/Introns: 80/1; 113/3; 154/2; 211/3; 273/2
C/Superfamily: Caenorhabditis elegans hypothetical protein T27A3.7

Query Match      91.2%; Score 31; DB 2; Length 373;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      262 CHALC 266

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RESULT 17
A69335
succinate dehydrogenase (EC 1.3.99.1) flavoprotein - Archaeoglobus fulgidus
C/Species: Archaeoglobus fulgidus
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
C/Accession: A69335
R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A/Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A/Reference number: A69250; MUID:98049343; PMID:9389475
A/Accession: A69335
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-563 <KLE>
A/Cross-references: UNIPROT:O29576; GB:AE01057; GB:AE000782; NID:g2689380; PIDN:AAB9055
C/Superfamily: Succinate dehydrogenase flavoprotein subunit; 3-oxosteroid 1-dehydrogenas
C/Keywords: FAD; flavoprotein; oxidoreductase
F:4-265/Domain: fumarate reductase flavoprotein homology <PRF>
F:297-389/Domain: 3-oxosteroid 1-dehydrogenase homology <OXD>

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Query Match      91.2%; Score 31; DB 2; Length 563;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      41 CHSVC 45

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RESULT 18
G87753
protein C43E11.8 [imported] - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G87753
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A/Reference number: A75000; MUID:99069613; PMID:9851916
A/Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A/Accession: G87753

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F;25-645/Domain: extracellular #status predicted <EXT>  
 F;75-300/Domain: EGF receptor extracellular domain repeat <EE1>  
 F;390-600/Domain: EGF receptor extracellular domain repeat <EE2>  
 F;646-668/Domain: transmembrane #status predicted <TM>  
 F;669-1210/Domain: intracellular #status predicted <INT>  
 F;710-975/Domain: protein kinase homology <KIN>  
 F;718-726/Region: protein kinase ATP-binding motif  
 F;999-1046/Region: coated-pit mediated internalization signal  
 F;1047-1210/Region: inhibitory  
 F;128,175,352,413,444,528,603/Binding site: carbohydrate (Asn)  
 F;745/Active site: Lys #status experimental

Query Match 91.2%; Score 31; DB 1; Length 1210;  
 Best Local Similarity 80.0%; Pred. No. 4.5e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 |||:  
 Db 506 CHALC 510

## RESULT 21

T34264

hypothetical protein F46C8.4 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*  
 C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
 C;Accession: T34264

R;Wilcox, L.

submitted to the EMBL Data Library, November 1995

A;Description: The sequence of *C. elegans* cosmid F46C8.

A;Reference number: Z21497

A;Accession: T34264

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-2195 <WIL>

A;Cross-references: EMBL:U41624; PIDN:AAA83316.1; CESP:F46C8.4

C;Genetics:

A;Gene: CESP:F46C8.4

A;Introns: 19/3; 61/3; 80/1; 159/1; 182/1; 208/2; 246/1; 308/1; 367/1; 422/1; 466/1; 507/29/3; 1721/3; 1767/3; 1811/1; 1874/1; 1920/1; 2011/2; 2068/3; 2117/1; 2161/1

Query Match 91.2%; Score 31; DB 2; Length 2195;  
 Best Local Similarity 80.0%; Pred. No. 6.9e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 |||:  
 Db 136 CHSVC 140

## RESULT 22

E96980

hypothetical protein CAC0655 [imported] - *Clostridium acetobutylicum*

C;Species: *Clostridium acetobutylicum*

C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004

C;Accession: E96980

R;Nolling, J.; Brston, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum*

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: E96980

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-67 <KUR>

A;Cross-references: UNIPROT:Q971A7; GB:AE001437; PIDN:AAK78632.1; PID:GI5023530; GSPDB:G

A;Experimental source: *Clostridium acetobutylicum* ATCC824

C;Genetics:

A;Gene: CAC0655

Query Match 88.2%; Score 30; DB 2; Length 67;  
 Best Local Similarity 80.0%; Pred. No. 84;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 |||:  
 Db 21 CHCVC 25

## RESULT 23

T25293

hypothetical protein T26E3.7 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T25293

R;Kershaw, J.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z20012

A;Accession: T25293

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-106 <WIL>

A;Cross-references: UNIPROT:O45827; EMBL:Z82053; PIDN:CAB04832.1; GSPDB:GN00019; CESP:T

A;Experimental source: clone T26E3

C;Genetics:

A;Gene: CESP:T26E3.7

A;Map position: 1

A;Introns: 81/2

Query Match 88.2%; Score 30; DB 2; Length 106;  
 Best Local Similarity 80.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 |||:  
 Db 53 CHVVC 57

## RESULT 24

AG2472

hypothetical protein alr5335 [imported] - *Nostoc* sp. (strain PCC 7120)

C;Species: *Nostoc* sp. PCC 7120

A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004

C;Accession: AG2472

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi;

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena*

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AG2472

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-108 <KUR>

A;Cross-references: UNIPROT:Q8VLG3; GB:BA000019; PIDN:BAW77034.1; PID:GI7134474; GSPDB:G

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: alr5335

Query Match 88.2%; Score 30; DB 2; Length 108;  
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 |||:  
 Db 11 CHSIC 15

## RESULT 25

AG2543

hypothetical protein alr7634 [imported] - *Nostoc* sp. (strain PCC 7120) plasmid pCC7120b6

C;Species: *Nostoc* sp. PCC 7120

A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004

C;Accession: AG2543

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi;

Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
 DNA Rep. 8, 205-213, 2001  
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena  
 A;Reference number: AB1807; MUID:21595285; PMID:11759840  
 A;Accession: AG2543  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-122 <KUR>  
 A;Cross-references: UNIPROT:Q8ZS78; GB:AP003602; PIDN:BA877277.1; PID:gl17134719; GSPDB:C  
 A;Experimental source: strain FCC 7120  
 C;Genetics:  
 A;Gene: alr7634  
 A;Genome: plasmid

Query Match  
 Best Local Similarity 88.2%; Score 30; DB 2; Length 122;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
 ||:|  
 Db 25 CHSIC 29

RESULT 26  
 A86086  
 hypothetical protein yijI [imported] - Escherichia coli (strain O157:H7, substrain EDL933)  
 C;Species: Escherichia coli  
 C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
 C;Accession: A86086  
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
 Nature 409, 529-533, 2001  
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A;Reference number: A85480; MUID:21074935; PMID:11206551  
 A;Accession: A86086  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-154 <STO>  
 A;Cross-references: UNIPROT:Q8X758; GB:AE005174; NID:gl2518866; PIDN:AAG59149.1; GSPDB:C  
 A;Experimental source: strain O157:H7, substrain EDL933  
 C;Genetics:  
 A;Gene: yijI

Query Match  
 Best Local Similarity 88.2%; Score 30; DB 2; Length 154;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
 ||:|  
 Db 86 CHSIC 90

RESULT 27  
 E91238  
 hypothetical protein ECs4876 [imported] - Escherichia coli (strain O157:H7, substrain R1  
 C;Species: Escherichia coli  
 C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
 C;Accession: E91238  
 R;Hayashi, T.; Makino, K.; Kurokawa, K.; Iehii, K.; Yokoyama, K.; Han, C.G.  
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
 A;Reference number: A99629; MUID:21156231; PMID:11258796  
 A;Accession: E91238  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-163 <HAY>  
 A;Cross-references: UNIPROT:Q8X758; GB:BA000007; PIDN:BA838300.1; PID:gl13364353; GSPDB:C  
 A;Experimental source: strain O157:H7, substrain R1MD 0509952  
 C;Genetics:  
 A;Gene: ECs4876

Query Match  
 Best Local Similarity 88.2%; Score 30; DB 2; Length 163;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 60.0%; Pred. No. 1.6e+02;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
 ||:|  
 Db 95 CHSIC 99

RESULT 28  
 T25841  
 hypothetical protein M03F4.6 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
 C;Accession: T25841  
 R;Fulton, L.  
 submitted to the EMBL Data Library, July 1996  
 A;Description: The sequence of C. elegans cosmid M03F4.  
 A;Reference number: Z20097  
 A;Accession: T25841  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-179 <FUL>  
 A;Cross-references: EMBL:U64601; PIDN:AAB04577.1; GSPDB:GN000028; CESP:M03F4.6  
 A;Experimental source: strain Bristol N2; clone M03F4  
 C;Genetics:  
 A;Gene: CESP:M03F4.6  
 A;Map position: X  
 A;introns: 41/1; 129/2

Query Match  
 Best Local Similarity 88.2%; Score 30; DB 2; Length 179;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5  
 ||:|  
 Db 38 CHATC 42

RESULT 29  
 IVHOA1  
 interferon alpha-I-1 precursor - horse  
 N;Alternate names: EqIFN-alpha-I-1; type I interferon  
 C;Species: Equus caballus (domestic horse)  
 C;Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 09-Jul-2004  
 C;Accession: A24912  
 R;Himmeler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.  
 DNA 5, 345-356, 1986  
 A;Title: Molecular cloning and expression in Escherichia coli of equine type I interferon  
 A;Reference number: A90956; MUID:87053170; PMID:3022999  
 A;Accession: A24912  
 A;Molecule type: DNA  
 A;Residues: 1-184 <HIM>  
 A;Cross-references: UNIPROT:P05003; GB:M14540; NID:gl64226; PIDN:AAA30953.1; PID:gl64227  
 C;Superfamily: interferon alpha  
 C;Keywords: antiviral  
 F;1-23/Domain: signal sequence #status predicted <SIG>  
 F;24-184/Product: interferon alpha-I-1 #status predicted <MAT>  
 F;24-122,52-162/Disulfide bonds: #status predicted

Query Match  
 Best Local Similarity 88.2%; Score 30; DB 1; Length 184;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
 ||:|  
 Db 16 CHSIC 20

RESULT 30  
 T34728  
 hypothetical protein SC1B6.07 - Streptomyces coelicolor  
 C;Species: Streptomyces coelicolor  
 C;Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004

C;Accession: T34728  
 R;Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, November 1998  
 A;Reference number: 221555  
 A;Accession: T34728  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-319 <SEE>  
 A;Cross-references: UNIPROT:Q92C15; EMBL:AL033505; PIDN:CAA22035.1; GSPDB:GN00070; SCOEI  
 A;Experimental source: strain A3(2)  
 C;Genetics:  
 C;Superfamily: Streptomyces coelicolor hypothetical protein SC4C6.19  
 A;Gene: SCOEI:SCIE6.07  
 Query Match 88.2%; Score 30; DB 2; Length 319;  
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 CHAVC 5  
 Db 111 CHTVC 115  
 RESULT 31  
 F70467  
 hypothetical protein aq\_1958 - Aquifex aeolicus  
 C;Species: Aquifex aeolicus  
 C;Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
 R;Accession: F70467  
 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O  
 V.  
 Nature 392, 353-358, 1998  
 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
 A;Reference number: A70300; MUID:98196666; PMID:9537320  
 A;Accession: F70467  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-372 <AOP>  
 A;Cross-references: UNIPROT:O67770; GB:AE000765; NID:g2984199; PIDN:AAC07741.1; PID:g298  
 A;Experimental source: strain VP5  
 C;Genetics:  
 A;Gene: aq\_1958  
 Query Match 88.2%; Score 30; DB 2; Length 372;  
 Best Local Similarity 80.0%; Pred. No. 2.9e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 CHAVC 5  
 Db 55 CHATC 59  
 RESULT 32  
 DEMSAA  
 alcohol dehydrogenase (EC 1.1.1.1) A - mouse  
 N;Alternate names: alcohol dehydrogenase beta  
 C;Species: Mus musculus (house mouse)  
 C;Date: 28-Feb-1986 #sequence\_revision 28-Feb-1986 #text\_change 09-Jul-2004  
 C;Accession: A27322; A29628; A00338; S50103; A25849  
 R;Zhang, K.; Bosron, W.F.; Edenberg, H.J.  
 Gene 57, 27-36, 1987  
 A;Title: Structure of the mouse Adh-1 gene and identification of a deletion in a long al  
 ty.  
 A;Reference number: A27322; MUID:98112859; PMID:3428612  
 A;Accession: A27322  
 A;Molecule type: DNA  
 A;Residues: 1-375 <ZHA>  
 A;Cross-references: UNIPROT:P00329; GB:M11307; NID:g191717; PIDN:AAA37180.1; PID:g309094  
 R;Ceci, J.D.; Zheng, Y.W.; Felder, M.R.  
 Gene 59, 171-182, 1987  
 A;Title: Molecular analysis of mouse alcohol dehydrogenase: nucleotide sequence of the A  
 A;Reference number: A29628; MUID:88137953; PMID:2893758  
 A;Accession: A29628

A;Molecule type: DNA  
 A;Residues: 1-375 <CEC>  
 A;Cross-references: GB:M22611  
 R;Edenberg, H.J.; Zhang, K.; Fong, K.; Bosron, W.F.; Li, T.K.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 2262-2266, 1985  
 A;Title: Cloning and sequencing of cDNA encoding the complete mouse liver alcohol dehydr  
 A;Reference number: A00338; MUID:85190477; PMID:3157987  
 A;Accession: A00338  
 A;Molecule type: mRNA  
 A;Residues: 1-375 <EDE>  
 A;Cross-references: GB:M11307; NID:g191717; PIDN:AAA37180.1; PID:g309094  
 A;Note: in Genbank entry MUSADH1A, release 109.0, the source is designated as Mus caroli  
 R;Cubán, J.; Iglesias, T.; Bernal, J.; Munoz, J.; Marquez, G.; Barbero, J.L.; Zaballón,  
 Nucleic Acids Res. 22, 4132-4138, 1994  
 A;Title: Isolation of genomic DNA fragments corresponding to genes modulated in vivo by  
 A;Reference number: S50102; MUID:95023181; PMID:7937138  
 A;Accession: S50103  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 8-51 <CAU>  
 A;Cross-references: EMBL:Z32540  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994  
 R;Ceci, J.D.; Lawther, R.; Duester, G.; Hatfield, G.W.; Smith, M.; O'Malley, M.P.; Felde  
 Gene 41, 217-224, 1986  
 A;Title: Androgen induction of alcohol dehydrogenase in mouse kidney. Studies with a cDN  
 A;Reference number: A25849; MUID:86221702; PMID:3011597  
 A;Accession: A25849  
 A;Molecule type: mRNA  
 A;Residues: 224-375 <CE2>  
 A;Cross-references: GB:M22611; NID:g191719; PIDN:AAA37181.1; PID:g191720  
 C;Comment: This enzyme converts primary and secondary alcohols to aldehydes using NAD as  
 C;Comment: The active enzyme is a dimer of identical or nonidentical zinc-containing pol  
 C;Genetics:  
 A;Gene: Adh-1  
 A;Introns: 6/3; 40/3; 87/1; 116/2; 189/3; 276/3; 322/1; 368/2  
 C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology  
 C;Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidor  
 F;2-375/Product: alcohol dehydrogenase chain A #status predicted <MAI>  
 F;32-366/Domain: long-chain alcohol dehydrogenase homology <LADH>  
 F;195-224/Region: beta-alpha-beta NAD nucleotide-binding fold  
 F;2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted  
 F;47,68,175/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted  
 F;98,101,104,112/Binding site: zinc, noncatalytic (Cys) #status predicted  
 Query Match 88.2%; Score 30; DB 1; Length 375;  
 Best Local Similarity 80.0%; Pred. No. 2.9e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 CHAVC 5  
 Db 283 CHAAC 287  
 RESULT 33  
 A39556  
 triacylglycerol lipase (EC 3.1.1.3) 2 - Moraxella sp. (strain TA144)  
 C;Species: Moraxella sp.  
 C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
 C;Accession: A39556  
 R;Feller, G.; Thriry, M.; Gerday, C.  
 DNA Cell Biol. 10, 381-388, 1991  
 A;Title: Nucleotide sequence of the lipase gene lip2 from the antarctic psychrotroph Mor  
 A;Reference number: A39556; MUID:91321741; PMID:1907455  
 A;Accession: A39556  
 A;Molecule type: DNA  
 A;Residues: 1-433 <FEL>  
 A;Cross-references: UNIPROT:P24484; GB:X53868; NID:g296841; PIDN:CAA37862.1; PID:g296842  
 C;Genetics:  
 A;Gene: lip2  
 C;Keywords: carboxylic ester hydrolase  
 Query Match 88.2%; Score 30; DB 2; Length 433;  
 Best Local Similarity 80.0%; Pred. No. 3.2e+02;

```

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CHAVC 5
      |||
Db      181 CHTVC 185

RESULT 34
S64826
Probable membrane protein YLR004c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein L1515
C:Species: Saccharomyces cerevisiae
C:Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: S64826
R:Vandenbol, M.; Portetelle, D.; Hilger, F.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64742
A:Accession: S64826
A:Molecule type: DNA
A:Residues: 1-523 <VAN>
A:Cross-references: UNIPROT:Q07904; EMBL:Z73176; NID:gl360291; PID:e245487; PID:gl360292
A:Experimental source: strain S288C
C:Genetics:
A:Gene: MIPS:YLR004c
A:Cross-references: SGD:S0003994
A:Map position: 12R
C:Keywords: transmembrane protein
F:78-94/Domain: transmembrane #status predicted <TM1>
F:123-139/Domain: transmembrane #status predicted <TM2>
F:147-163/Domain: transmembrane #status predicted <TM3>
F:242-258/Domain: transmembrane #status predicted <TM4>
F:345-361/Domain: transmembrane #status predicted <TM5>
F:379-395/Domain: transmembrane #status predicted <TM6>
F:467-483/Domain: transmembrane #status predicted <TM7>

Query Match      88.2%; Score 30; DB 2; Length 523;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CHAVC 5
      |||
Db      161 CHAAC 165

RESULT 35
F86281
protein F10B6.14 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: F86281
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
ansen, N.F.; Hughes, B.; Huizlar, L.
Nature 408, 816-820, 2000
C:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luroe, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.B.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F86281
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-760 <STO>
A:Cross-references: UNIPROT:Q9LQV7; GB:AE005172; NID:g8778236; PIDN:AAF79245.1; GSPDB:GN
C:Genetics:
A:Gene: F10B6.14
A:Map position: 1

Query Match      88.2%; Score 30; DB 2; Length 760;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 CHAVC 5
      |||
Db      464 CHAAC 468

```

## RESULT 36

```

S55554
male-specific lethal 2 protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S55554
R:Zhou, S.; Yang, Y.; Scott, M.J.; Panmuti, A.; Fehr, K.C.; Eisen, A.; Koonin, E.V.; Fout
EMBO J. 14, 2894-2895, 1995
A:Title: Male-specific lethal 2, a dosage compensation gene of Drosophila, undergoes sex
A:Reference number: S55554; MUID:95317307; PMID:7796814
A:Accession: S55554
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-769 <ZHO>
A:Cross-references: UNIPROT:P50534; EMBL:Z48443; NID:g872110; PIDN:CAA88358.1; PID:g87211
C:Genetics:
A:Gene: FlyBase:mel-2
A:Cross-references: FlyBase:FBgn0005616
A:Introns: 641/1

```

```

Query Match      88.2%; Score 30; DB 2; Length 769;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 CHAVC 5
      |||
Db      552 CHCVC 556

```

## RESULT 37

```

A27131
epidermal growth factor receptor - fruit fly (Drosophila melanogaster) (fragment)
C:Species: Drosophila melanogaster
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: A27131
R:Schejter, E.D.; Segal, D.; Glazer, L.; Shilo, B.2.
Cell 46, 1091-1101, 1986
A:Title: Alternative 5' exons and tissue-specific expression of the Drosophila EGF receptor
A:Reference number: A27131; MUID:87002474; PMID:3093080
A:Accession: A27131
A:Molecule type: mRNA
A:Residues: 1-843 <SCH>
A:Cross-references: UNIPROT:Q8MLW0
C:Genetics:
A:Gene: FlyBase:Egfr
A:Cross-references: FlyBase:FBgn0003731
A:Superfamily: epidermal growth factor receptor; protein kinase homology
C:Keywords: ATP; growth factor receptor

```

```

Query Match      88.2%; Score 30; DB 2; Length 843;
Best Local Similarity 80.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 CHAVC 5
      |||
Db      619 CHATC 623

```

## RESULT 38

```

B81704
conserved hypothetical protein TC024 [imported] - Chlamydia muridarum (strain Nigg)
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: B81704
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.P.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000

```

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
A;Reference number: A81500; UID:20150255; PMID:10684935  
A;Accession: B81704  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1436 <ET>  
A;Cross-references: UNIPROT:Q9PKP1; GB:AE002309; GB:AE002160; NID:g7190464; PIDN:AAF3928  
A;Experimental source: strain Nigg (MoPn)  
C;Genetics:  
A;Gene: TC0424

Query Match 88.2%; Score 30; DB 2; Length 1436;  
Best Local Similarity 80.0%; Pred. No. 7.6e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
||| |  
Db 1033 CHAAC 1037

RESULT 39  
VGIH23  
E2 glycoprotein precursor - porcine transmissible gastroenteritis virus (strain Purdue)  
N;Alternate names: peplomer protein; spike glycoprotein  
C;Species: porcine transmissible gastroenteritis virus  
C;Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 12-Apr-1996  
C;Accession: J50336  
R;Jacobs, L.; de Groot, R.; van der Zeijst, B.A.M.; Horzinek, M.C.; Spaan, W.  
Virus Res. 8, 363-371, 1987  
A;Title: The nucleotide sequence of the peplomer gene of porcine transmissible gastroenteritis virus (FIPV).  
A;Reference number: J50336; UID:88129049; PMID:2829461  
A;Accession: J50336  
A;Molecule type: mRNA  
A;Residues: 1-1447 <JAC>  
C;Superfamily: coronavirus E2 glycoprotein  
C;Keywords: glycoprotein; transmembrane protein  
F;1-16/Domain: signal sequence #status predicted <SIG>  
F;17-1447/Product: E2 glycoprotein #status predicted <MAT>  
F;1397-1431/Domain: transmembrane #status predicted <TM>  
F;26,42,71,94,243,250,285,334,345,362,403,447,514,530,552,592,702,723,778,817,832,838,91  
F;26,42,71,94,243,250,285,334,345,362,403,447,514,530,552,592,702,723,778,817,832,838,91

Query Match 88.2%; Score 30; DB 1; Length 1447;  
Best Local Similarity 60.0%; Pred. No. 7.6e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
||| |  
Db 1426 CHSIC 1430

RESULT 40  
VGIH2  
E2 glycoprotein precursor - porcine transmissible gastroenteritis virus (strain Purdue-1)  
N;Alternate names: spike glycoprotein  
C;Species: porcine transmissible gastroenteritis virus  
A;Variety: strain purdue-115  
C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004  
C;Accession: A27106; S01738  
R;Raschaert, D.; Laude, H.  
J. Gen. Virol. 68, 1883-1890, 1987  
A;Title: The predicted primary structure of the peplomer protein E2 of the porcine coronavirus.  
A;Reference number: A27106; UID:87253116; PMID:3037011  
A;Accession: A27106  
A;Molecule type: genomic RNA  
A;Residues: 1-1447 <RAS>  
A;Cross-references: UNIPROT:P07946; GB:X05695; GB:D00118; NID:g59007; PIDN:CAA29175.1; F;1-1447/Domain: signal sequence #status predicted <SIG>  
R;Raschaert, D.; Gelfi, J.; Laude, H.  
Biochimie 69, 591-600, 1987  
A;Title: Enteric coronavirus TGEV: partial sequence of the genomic RNA, its organization  
A;Reference number: S01738; UID:88078100; PMID:2825819  
A;Accession: S01738

A;Molecule type: genomic RNA  
A;Residues: 1434-1447 <RAW>  
A;Cross-references: EMBL:X06371  
A;Experimental source: strain Purdue-115  
C;Superfamily: coronavirus E2 glycoprotein  
C;Keywords: glycoprotein; transmembrane protein  
F;1-16/Domain: signal sequence #status predicted <SIG>  
F;17-1447/Product: E2 glycoprotein #status predicted <MAT>  
F;1387-1431/Domain: transmembrane #status predicted <TM>  
F;26,42,71,94,243,250,285,334,345,362,403,447,514,530,552,592,702,723,778,817,832,838,91

Query Match 88.2%; Score 30; DB 1; Length 1447;  
Best Local Similarity 60.0%; Pred. No. 7.6e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
||| |  
Db 1426 CHSIC 1430

RESULT 41  
A43573  
E2 glycoprotein precursor - porcine transmissible gastroenteritis virus (strain Miller)  
N;Alternate names: peplomer glycoprotein; spike glycoprotein  
C;Species: porcine transmissible gastroenteritis virus  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: A43573  
R;Weasley, R.D.  
Adv. Exp. Med. Biol. 276, 301-306, 1990  
A;Title: Nucleotide sequence of the E2-peplomer protein gene and partial nucleotide sequence of the E2-peplomer protein gene (strain Miller).  
A;Reference number: A43573; UID:91353366; PMID:1966416  
A;Accession: A43573  
A;Molecule type: genomic RNA  
A;Residues: 1-1449 <WES>  
A;Cross-references: UNIPROT:P33470; GB:S51223; NID:g234109; PIDN:AAB19567.1; PID:g234110  
A;Note: the authors translated the codon GAA for residue 388 as Cys  
C;Superfamily: coronavirus E2 glycoprotein  
C;Keywords: glycoprotein; transmembrane protein  
F;1-16/Domain: signal sequence #status predicted <SIG>  
F;17-1449/Product: E2 glycoprotein #status predicted <E2G>  
F;1027-1043/Region: hydrophobic  
F;1391-1411/Domain: transmembrane #status predicted <TM>  
F;26,42,71,94,243,250,285,334,345,362,375,405,449,516,532,554,594,704,725,780,819,834,84  
F;26,42,71,94,243,250,285,334,345,362,375,405,449,516,532,554,594,704,725,780,819,834,84

Query Match 88.2%; Score 30; DB 1; Length 1449;  
Best Local Similarity 60.0%; Pred. No. 7.6e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
||| |  
Db 1428 CHSIC 1432

RESULT 42  
VGIHFS  
E2 glycoprotein precursor - porcine transmissible gastroenteritis virus (strain FS772/70)  
N;Alternate names: peplomer glycoprotein; spike glycoprotein  
C;Species: porcine transmissible gastroenteritis virus  
C;Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 09-Jul-2004  
C;Accession: B43489; S11728  
R;Britton, P.; Page, K.W.  
Virus Res. 18, 71-80, 1990  
A;Title: Sequence of the S gene from a virulent British field isolate of transmissible gastroenteritis virus.  
A;Reference number: A43489; UID:91188698; PMID:1964522  
A;Accession: B43489  
A;Molecule type: mRNA  
A;Residues: 1-1449 <BRI>  
A;Cross-references: UNIPROT:P18450; GB:X53128; NID:g61377; PIDN:CAA37285.1; PID:g61379  
C;Superfamily: coronavirus E2 glycoprotein  
C;Keywords: glycoprotein; transmembrane protein  
F;1-16/Domain: signal sequence #status predicted <SIG>  
F;17-1449/Product: E2 glycoprotein #status predicted <E2G>

F;1027-1043/region: hydrophobic  
F;1395-1411/Domain: transmembrane #status predicted <TM>  
F;26,42,71,94,243,250,285,334,345,362,375,405,449,516,532,554,594,704,725,780,819,834,844  
d

Query Match 88.2%; Score 30; DB 1; Length 1449;  
Best Local Similarity 60.0%; Pred. No. 7.6e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
||:|  
Db 1428 CHSIC 1432

RESULT 43  
S47423  
E2 glycoprotein precursor - porcine transmissible gastroenteritis virus  
N;Alternate names: envelope protein; spike protein  
C;Species: porcine transmissible gastroenteritis virus  
C;Date: 23-Nov-1994 #sequence\_revision 19-Apr-1996 #text\_change 09-Jul-2004  
C;Accession: S65851; S47423  
R;Chen, C.M.; Cavanagh, D.; Britton, P.  
Virus Res. 38, 83-89, 1995  
A;Title: Cloning and sequencing of a 8.4-kb region from the 3'-end of a Taiwanese viru  
A;Reference number: S65850; MUID:96060227; PMID:8546012  
A;Accession: S65851  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: genomic RNA  
A;Residues: 1-1449 <CH2>  
A;Cross-references: UNIPROT:Q88510; EMBL:Z35759; NID:G529246; PIDN:CAA84806.1; PID:G5292  
A;Experimental source: Taiwanese field isolate  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994  
C;Genetics:  
A;Gene: S  
C;Superfamily: coronavirus E2 glycoprotein  
C;Keywords: glycoprotein; transmembrane protein  
F;1-16/Domain: signal sequence #status predicted <SIG>  
F;17-1449/Product: E2 glycoprotein #status predicted <E2G>

Query Match 88.2%; Score 30; DB 2; Length 1449;  
Best Local Similarity 60.0%; Pred. No. 7.6e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
||:|  
Db 1428 CHSIC 1432

RESULT 44  
JQ1719  
E2 glycoprotein precursor - canine coronavirus (strain Insvac-1)  
N;Alternate names: spike glycoprotein  
C;Species: canine coronavirus  
C;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004  
C;Accession: JQ1719  
R;Horsburgh, B.C.; Brierley, I.; Brown, T.D.K.  
J. Gen. Virol. 73, 2849-2862, 1992  
A;Title: Analysis of a 9.6 kb sequence from the 3' end of canine coronavirus genomic RNA  
A;Reference number: PQ0481; MUID:93057357; PMID:1431811  
A;Accession: JQ1719  
A;Molecule type: genomic RNA  
A;Residues: 1-1451 <HOR>  
A;Cross-references: UNIPROT:P36300; DBJ:DJ13096; NID:G406193; PIDN:BA02408.1; PID:G4061  
C;Genetics:  
A;Gene: S  
C;Superfamily: coronavirus E2 glycoprotein  
C;Keywords: glycoprotein; transmembrane protein  
F;1-18/Domain: signal sequence #status predicted <SIG>  
F;19-1451/Product: spike glycoprotein #status predicted <MAT>  
F;1394-1412/Domain: transmembrane #status predicted <TM>  
F;28,66,94,142,175,209,235,242,289,338,349,366,379,409,453,520,536,557,707,728,783,821,8  
d

Query Match 88.2%; Score 30; DB 1; Length 1451;  
Best Local Similarity 60.0%; Pred. No. 7.6e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
||:|  
Db 1430 CHSIC 1434

RESULT 45  
VG1H79  
E2 glycoprotein precursor - feline infectious peritonitis virus (strain 79-1146)  
N;Alternate names: peplomer glycoprotein; spike glycoprotein  
C;Species: feline infectious peritonitis virus  
C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C;Accession: A27171  
R;De Groot, R.J.; Maduro, J.; Lenstra, J.A.; Horzinek, M.C.; Van Der Zeijst, B.A.M.; Spa  
J. Gen. Virol. 68, 2639-2646, 1987  
A;Title: cDNA cloning and sequence analysis of the gene encoding the peplomer protein of  
A;Reference number: A27171; MUID:88034948; PMID:3312491  
A;Accession: A27171  
A;Molecule type: genomic RNA  
A;Residues: 1-1452 <DEG>  
A;Cross-references: UNIPROT:P10033; GB:X06170; GB:D00150; NID:G58915; PIDN:CAA29535.1; P  
C;Superfamily: coronavirus E2 glycoprotein  
C;Keywords: glycoprotein; transmembrane protein  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;19-1452/Product: spike glycoprotein #status predicted <TM>  
F;1394-1414/Domain: transmembrane #status predicted <TM2>  
F;29,95,174,208,234,241,288,337,348,365,408,452,483,519,535,557,565,707,728,783,822,837,8  
ted

Query Match 88.2%; Score 30; DB 1; Length 1452;  
Best Local Similarity 60.0%; Pred. No. 7.6e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
||:|  
Db 1431 CHSIC 1435

RESULT 46  
S41453  
spike protein - canine coronavirus  
C;Species: canine coronavirus  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S41453  
R;Wesseling, J.G.; Vennema, H.; Godeke, G.J.; Spaan, W.J.M.; Horzinek, M.C.; Rottier, P.  
submitted to the EMBL Data Library, December 1993  
A;Description: Nucleotide sequence and expression of the spike (S) gene of canine coronav  
A;Reference number: S41453  
A;Accession: S41453  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1453 <WES>  
A;Cross-references: UNIPROT:Q65984; EMBL:X77047; NID:G452379; PIDN:CAA54335.1; PID:G4523  
C;Superfamily: coronavirus E2 glycoprotein

Query Match 88.2%; Score 30; DB 2; Length 1453;  
Best Local Similarity 60.0%; Pred. No. 7.6e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
||:|  
Db 1432 CHSIC 1436

RESULT 47  
A42125  
trophozoite cysteine-rich surface antigen 170 - Giardia lamblia  
N;Alternate names: CRP170; cysteine-rich surface antigen CRP170  
C;Species: Giardia lamblia

C;Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 09-Jul-2004  
 C;Accession: A42125; B42125; S00530; S48056  
 R;Adam, R.D.; Yang, Y.M.; Nash, T.E.  
 Mol. Cell. Biol. 12, 1194-1201, 1992  
 A;Title: The cysteine-rich protein gene family of Giardia lamblia: loss of the CRP170 gene  
 A;Reference number: A42125; MUID:92186850; PMID:1545800  
 A;Accession: A42125  
 A;Molecule type: DNA  
 A;Residues: 1-98 <ADA1>  
 A;Cross-references: UNIPROT:P15799; GB:M83937; NID:g159124  
 A;Experimental source: trophozoite  
 A;Note: sequence extracted from NCBI backbone (NCBIN:88421, NCBIP:88427); this ORF is not  
 A;Note: the authors report but do not show 19 tandem repeats of the sequence of residues  
 A;Accession: B42125  
 A;Molecule type: DNA  
 A;Residues: 1269-1766 <ADA2>  
 A;Cross-references: GB:M83933; NID:g159122  
 A;Note: sequence extracted from NCBI backbone (NCBIN:88424, NCBIP:88431); this ORF is not  
 R;Adam, R.D.; Aggarwal, A.; Lal, A.A.; de la Cruz, V.F.; McCutchan, T.; Nash, T.E.  
 J. Exp. Med. 167, 109-118, 1988  
 A;Title: Antigenic variation of a cysteine-rich protein in Giardia lamblia.  
 A;Reference number: S00530; MUID:88089405; PMID:3335828  
 A;Accession: S00530  
 A;Molecule type: DNA  
 A;Residues: 1154-1409, 'A', 1411-1420, 'K', 1422-1425, 'R', 1427-1481 <ADA3>  
 A;Cross-references: EMBL:X06741; NID:g93355; PID:g929603  
 R;Yang, Y.; Adam, R.D.  
 Nucleic Acids Res. 22, 2102-2108, 1994  
 A;Title: Allele-specific expression of a variant-specific surface protein (VSP) of Giardia  
 A;Reference number: S48056; MUID:94301794; PMID:8029018  
 A;Accession: S48056  
 A;Molecule type: DNA  
 A;Residues: 1-56 <VAN>  
 A;Cross-references: EMBL:L25059  
 A;Experimental source: trophozoites WBA6  
 A;Note: the source is designated as Giardia intestinalis  
 C;Comment: This translation was produced by PIR staff from information provided by the a  
 C;Genetics:  
 A;Gene: VSPA6  
 C;Keywords: surface antigen; tandem repeat

Query Match 88.2%; Score 30; DB 2; Length 1766;  
 Best Local Similarity 80.0%; Pred. No. 8.8e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 |||  
 Db 1504 CHATC 1508

RESULT 48  
 B96981  
 hypothetical protein CAC0660 [imported] - Clostridium acetobutylicum  
 C;Species: Clostridium acetobutylicum  
 C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
 C;Accession: B96981  
 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
 J. Bacteriol. 183, 4823-4838, 2001  
 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo  
 A;Reference number: A96900; MUID:21359325; PMID:21359325  
 A;Accession: B96981  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-67 <KUR>  
 A;Cross-references: UNIPROT:Q97LA2; GB:AE001437; PIDN:AAK78637.1; PID:g15023535; GSPDB:G  
 A;Experimental source: Clostridium acetobutylicum ATCC824  
 C;Genetics:  
 A;Gene: CAC0660

Query Match 85.3%; Score 29; DB 2; Length 67;  
 Best Local Similarity 60.0%; Pred. No. 1.3e+02;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

C;Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 09-Jul-2004  
 C;Accession: A42125; B42125; S00530; S48056  
 R;Adam, R.D.; Yang, Y.M.; Nash, T.E.  
 Mol. Cell. Biol. 12, 1194-1201, 1992  
 A;Title: The cysteine-rich protein gene family of Giardia lamblia: loss of the CRP170 ge  
 A;Reference number: A42125; MUID:92186850; PMID:1545800  
 A;Accession: A42125  
 A;Molecule type: DNA  
 A;Residues: 1-98 <ADA1>  
 A;Cross-references: UNIPROT:P15799; GB:M83937; NID:g159124  
 A;Experimental source: trophozoite  
 A;Note: sequence extracted from NCBI backbone (NCBIN:88421, NCBIP:88427); this ORF is not  
 A;Note: the authors report but do not show 19 tandem repeats of the sequence of residues  
 A;Accession: B42125  
 A;Molecule type: DNA  
 A;Residues: 1269-1766 <ADA2>  
 A;Cross-references: GB:M83933; NID:g159122  
 A;Note: sequence extracted from NCBI backbone (NCBIN:88424, NCBIP:88431); this ORF is not  
 R;Adam, R.D.; Aggarwal, A.; Lal, A.A.; de la Cruz, V.F.; McCutchan, T.; Nash, T.E.  
 J. Exp. Med. 167, 109-118, 1988  
 A;Title: Antigenic variation of a cysteine-rich protein in Giardia lamblia.  
 A;Reference number: S00530; MUID:88089405; PMID:3335828  
 A;Accession: S00530  
 A;Molecule type: DNA  
 A;Residues: 1154-1409, 'A', 1411-1420, 'K', 1422-1425, 'R', 1427-1481 <ADA3>  
 A;Cross-references: EMBL:X06741; NID:g93355; PID:g929603  
 R;Yang, Y.; Adam, R.D.  
 Nucleic Acids Res. 22, 2102-2108, 1994  
 A;Title: Allele-specific expression of a variant-specific surface protein (VSP) of Giardia  
 A;Reference number: S48056; MUID:94301794; PMID:8029018  
 A;Accession: S48056  
 A;Molecule type: DNA  
 A;Residues: 1-56 <VAN>  
 A;Cross-references: EMBL:L25059  
 A;Experimental source: trophozoites WBA6  
 A;Note: the source is designated as Giardia intestinalis  
 C;Comment: This translation was produced by PIR staff from information provided by the a  
 C;Genetics:  
 A;Gene: VSPA6  
 C;Keywords: surface antigen; tandem repeat

Query Match 88.2%; Score 30; DB 2; Length 1766;  
 Best Local Similarity 80.0%; Pred. No. 8.8e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 |||  
 Db 1504 CHATC 1508

RESULT 48  
 B96981  
 hypothetical protein CAC0660 [imported] - Clostridium acetobutylicum  
 C;Species: Clostridium acetobutylicum  
 C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
 C;Accession: B96981  
 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
 J. Bacteriol. 183, 4823-4838, 2001  
 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo  
 A;Reference number: A96900; MUID:21359325; PMID:21359325  
 A;Accession: B96981  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-67 <KUR>  
 A;Cross-references: UNIPROT:Q97LA2; GB:AE001437; PIDN:AAK78637.1; PID:g15023535; GSPDB:G  
 A;Experimental source: Clostridium acetobutylicum ATCC824  
 C;Genetics:  
 A;Gene: CAC0660

Query Match 85.3%; Score 29; DB 2; Length 67;  
 Best Local Similarity 60.0%; Pred. No. 1.3e+02;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 |||  
 Db 21 CHGIC 25

## RESULT 49

T27516  
 hypothetical protein ZC334.2 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T27516  
 R;McLay, K.  
 submitted to the EMBL Data Library, November 1996  
 A;Reference number: Z20381  
 A;Accession: T27516  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-120 <WIL>  
 A;Cross-references: UNIPROT:Q9XUI8; EMBL:Z82082; PIDN:CA804963.1; GSPDB:GN00019; CESP:ZC  
 A;Experimental source: clone ZC334  
 C;Genetics:  
 A;Gene: CESP:ZC334.2  
 A;Map position: 1  
 A;Introns: 90/1

Query Match 85.3%; Score 29; DB 2; Length 120;  
 Best Local Similarity 60.0%; Pred. No. 1.9e+02;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 |||  
 Db 80 CHGIC 84

## RESULT 50

Q0EC30  
 prepilin peptidase dependent protein B precursor - Escherichia coli (strain K-12)  
 C;Species: Escherichia coli  
 C;Date: 31-Mar-1988 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
 C;Accession: B65065; C24137  
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
 .A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A;Title: The complete genome sequence of Escherichia coli K-12.  
 A;Reference number: A64720; MUID:97426617; PMID:9278503  
 A;Accession: B65065  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-187 <BLAT>  
 A;Cross-references: UNIPROT:P08371; GB:AE000366; GB:U00096; NID:g1789185; PIDN:AACT5864.  
 A;Experimental source: strain K-12, substrain MG1655  
 R;Finch, P.W.; Wilson, R.E.; Brown, K.; Hickson, I.D.; Tomkinson, A.E.; Emmerson, P.T.  
 Nucleic Acids Res. 14, 4437-4451, 1986  
 A;Title: Complete nucleotide sequence of the Escherichia coli recC gene and of the thyA-  
 A;Reference number: A93625; MUID:86232583; PMID:3520484  
 A;Accession: C24137  
 A;Molecule type: DNA  
 A;Residues: 'M'PCSPRCWGQYLSNQFTIGLCATLARSNERPDTPACFLWPAQVHMGRAYSLOKLNKRVVAGGFAVGKTPALS;  
 A;Cross-references: GB:X03966; NID:g42684; PIDN:CAA27601.1; PID:g42686  
 C;Genetics:  
 A;Gene: ppdB  
 A;Map position: 61 min  
 C;Superfamily: prepilin peptidase dependent protein B precursor

Query Match 85.3%; Score 29; DB 1; Length 187;  
 Best Local Similarity 60.0%; Pred. No. 2.6e+02;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 |||  
 Db 68 CHGIC 72



```

RESULT 51
D85934
Prepilin peptidase dependent protein B [imported] - Escherichia coli (strain O157:H7, su
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: D85934
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: D85934
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-187 <STO>
A:Cross-references: UNIPROT:Q8X6M2; GB:AE005174; NID:g12517110; PIDN:AAG57936.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain BDL933
C:Genetics:
A:Gene: ppeB
C:Superfamily: prepilin peptidase dependent protein B precursor

Query Match      85.3%; Score 29; DB 2; Length 187;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 CHAVC 5
      ||| :|
Db      68 CHGIC 72

RESULT 52
B98089
Prepilin peptidase dependent protein B [imported] - Escherichia coli (strain O157:H7, su
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: B98089
R:Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Iehli, K.; Yokoyama, K.; Han, C.G.
gaesawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: B98089
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-187 <HAY>
A:Cross-references: UNIPROT:Q8X6M2; GB:BA000007; PIDN:BAB37105.1; PID:g13363154; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECe3682
C:Superfamily: prepilin peptidase dependent protein B precursor

Query Match      85.3%; Score 29; DB 2; Length 187;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 CHAVC 5
      ||| :|
Db      68 CHGIC 72

RESULT 53
G71343
hypothetical protein TP0284 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: G71343
R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876

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A:Accession: G71343
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-219 <COI>
A:Cross-references: UNIPROT:O83308; GB:AE001209; GB:AE000520; NID:g3322547; PIDN:AAC6528
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0284
C:Superfamily: syphilis spirochete hypothetical protein TP0284

Query Match      85.3%; Score 29; DB 2; Length 219;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CHAVC 5
      ||| ||
Db      76 CHQVC 80

RESULT 54
A82147
ABC transporter, ATP-binding protein VC1883 [imported] - Vibrio cholerae (strain N16961
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: A82147
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: A82147
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-228 <HEI>
A:Cross-references: UNIPROT:P57066; GB:AE004263; GB:AE003852; NID:g9656399; PIDN:AAF95031
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1883
A:Map position: 1
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match      85.3%; Score 29; DB 2; Length 228;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CHAVC 5
      ||| ||
Db      7 CHQVC 11

RESULT 55
S76342
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S76342
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76342
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-234 <KAN>
A:Cross-references: UNIPROT:O57208; EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAA1019-
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: Mg2+-transporting ATPase

Query Match      85.3%; Score 29; DB 2; Length 234;

```



Best Local Similarity 80.0%; Pred. No. 3.1e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

Qy 1 CHAVC 5  
|||  
Db 149 CHLVC 153

RESULT 56  
F72426  
iron-sulfur cluster-binding protein - Thermotoga maritima (strain MSB8)  
C:Species: Thermotoga maritima  
C>Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 16-Aug-2004  
C:Accession: F72426  
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;  
C.M.

Nature 399, 323-329, 1999  
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq  
A:Reference number: A72200; MUID:99287316; PMID:10360571  
A:Accession: F72426  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-261 <ARN>  
A:Cross-references: UNIPROT:Q9WXQ6; GB:AE001691; GB:AE000512; NID:g94980517; PIDN:AAD3514  
A:Experimental source: strain MSB8  
C:Genetics:  
A:Gene: TM0049  
C:Superfamily: ferredoxin 2(4Fe-4S) homology

Query Match 85.3%; Score 29; DB 2; Length 261;  
Best Local Similarity 80.0%; Pred. No. 3.3e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

Qy 1 CHAVC 5  
|||  
Db 245 CHEVC 249

RESULT 57  
T17632  
hypothetical protein al41L - Chlorella virus PBCV-1  
C:Species: Chlorella virus PBCV-1  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T17632  
R:Graves, M.V.; Van Etten, J.L.  
submitted to the EMBL Data Library, May 1999  
A:Reference number: Z18806  
A:Accession: T17632  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-265 <GRA>  
A:Cross-references: UNIPROT:Q84461; EMBL:U42580; NID:g4028996; PIDN:AAC96509.1  
A:Experimental source: specific host Chlorella strain NC64A  
C:Genetics:  
A:Note: al41L

Query Match 85.3%; Score 29; DB 2; Length 265;  
Best Local Similarity 60.0%; Pred. No. 3.4e+02; Mismatches 1; Indels 0; Gaps 0;  
Matches 3; Conservative 1;

Qy 1 CHAVC 5  
|||  
Db 256 CHGIC 260

RESULT 58  
T52387  
hypothetical protein MWB12.6 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 24-Oct-2000 #sequence\_revision 24-Oct-2000 #text\_change 09-Jul-2004  
C:Accession: T52387  
R:Kaneko, T.; Kato, T.; Sato, S.; Nakamura, Y.; Asamizu, E.; Tabata, S.

submitted to the EMBL Data Library, September 1999  
A:Reference number: Z26062  
A:Accession: T52387  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-307 <KAN>  
A:Cross-references: UNIPROT:Q9LJN7; EMBL:AP000417; PIDN:BA02544.1  
A:Experimental source: cultivar Columbia  
C:Genetics:  
A:Map position: 3

Query Match 85.3%; Score 29; DB 2; Length 307;  
Best Local Similarity 60.0%; Pred. No. 3.7e+02; Mismatches 1; Indels 0; Gaps 0;  
Matches 3; Conservative 1;

Qy 1 CHAVC 5  
|||  
Db 41 CHGIC 45

## RESULT 59

I40700  
type II site-specific deoxyribonuclease (EC 3.1.21.4) Cfr9I - Citrobacter freundii  
C:Species: Citrobacter freundii  
C>Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: I40700; S37179  
R:Lubys, A.; Menkevicius, S.; Timinskas, A.; Butkus, V.; Janulaitis, A.  
Gene 141, 85-89, 1994  
A:Title: Cloning and analysis of translational control for genes encoding the Cfr9I reat  
A:Reference number: I40699; MUID:94215893; PMID:8163180  
A:Accession: I40700  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-330 <RES>  
A:Cross-references: UNIPROT:Q60132; EMBL:X74517; NID:g402178; PIDN:CAAS2628.1; PID:g4021

## C:Genetics:

A:Gene: cfr9IR

C:Keywords: hydrolase

Query Match 85.3%; Score 29; DB 2; Length 330;  
Best Local Similarity 80.0%; Pred. No. 3.9e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

Qy 1 CHAVC 5  
|||  
Db 131 CHAFC 135

## RESULT 60

A64378  
hypothetical protein MJ0625 - Methanococcus jannaschii

C:Species: Methanococcus jannaschii

C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004

C:Accession: A64378

R:Buit, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, A.; Reich, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C

A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii

A:Reference number: A64300; MUID:96337999; PMID:8688087

A:Accession: A64378

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-336 <BUL>

A:Cross-references: UNIPROT:Q58042; GB:U67510; NID:g1591325; PIDN:AAB98625.1;

C:Genetics:

A:Map position: FOR553608-554618

C:Superfamily: ATP-binding protein PAB1945

Query Match 85.3%; Score 29; DB 2; Length 336;

Best Local Similarity 60.0%; Pred. No. 4e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 3; Conservative 1;

QY 1 CHAVC 5  
 Db 168 CHVIC 172

RESULT 61  
 C64434  
 hypothetical protein MJ1076 - Methanococcus jannaschii  
 C:Species: Methanococcus jannaschii  
 C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
 C:Accession: C64434  
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, A.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
 Science 273, 1058-1073, 1996  
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.  
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii  
 A:Reference number: A64300; MUID:96337999; PMID:8688087  
 A:Accession: C64434  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-337 <BUL>  
 A:Cross-references: UNIPROT:Q58476; GB:U67550; GB:L77117; NID:g1591722; PIDN:AAB99081.1;  
 C:Genetics:  
 A:Map position: REV1016648-1015635  
 C:Superfamily: ATP-binding protein PAB1945

Query Match 85.3%; Score 29; DB 2; Length 337;  
 Best Local Similarity 60.0%; Pred. No. 4e+02;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5  
 Db 168 CHVIC 172

RESULT 62  
 C64513  
 hypothetical protein MJECL26 - Methanococcus jannaschii plasmid pURB800  
 C:Species: Methanococcus jannaschii  
 C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
 C:Accession: A64513  
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, A.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
 Science 273, 1058-1073, 1996  
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.  
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii  
 A:Reference number: A64300; MUID:96337999; PMID:8688087  
 A:Accession: A64513  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-343 <BUL>  
 A:Cross-references: UNIPROT:Q60285; GB:L77118; NID:g1500644; TIGR:MJECL26; PIDN:AAC37097  
 C:Genetics:  
 A:Map position: ECLREV30206-23175  
 A:Genome: plasmid  
 A:Start codon: TTG  
 A:Note: this stable 58-kilobase pair plasmid is also designated ECL (large extrachromosomal)  
 C:Superfamily: ATP-binding protein PAB1945

Query Match 85.3%; Score 29; DB 2; Length 343;  
 Best Local Similarity 60.0%; Pred. No. 4e+02;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5  
 Db 172 CHVIC 176

RESULT 63  
 E64425  
 hypothetical protein MJ1006 - Methanococcus jannaschii  
 C:Species: Methanococcus jannaschii  
 C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
 C:Accession: E64425  
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, A.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
 Science 273, 1058-1073, 1996  
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.  
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii  
 A:Reference number: A64300; MUID:96337999; PMID:8688087  
 A:Accession: E64425  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-359 <BUL>  
 A:Cross-references: UNIPROT:Q58412; GB:U67543; GB:L77117; NID:g1591663; PIDN:AAB99014.1;  
 C:Genetics:  
 A:Map position: FOR934363-935442  
 A:Start codon: TTG  
 C:Superfamily: ATP-binding protein PAB1945

Query Match 85.3%; Score 29; DB 2; Length 359;  
 Best Local Similarity 60.0%; Pred. No. 4.2e+02;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5  
 Db 190 CHVIC 194

RESULT 64  
 H87344  
 esterase, probable [imported] - Caulobacter crescentus  
 C:Species: Caulobacter crescentus  
 C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
 C:Accession: H87344  
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.J.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonski, J.; Emolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
 A:Title: Complete Genome Sequence of Caulobacter crescentus.  
 A:Reference number: A87249; MUID:21173698; PMID:11259647  
 A:Accession: H87344  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-380 <STO>  
 A:Cross-references: UNIPROT:Q9AA37; GB:AE005673; NID:g13422010; PIDN:AAK22756.1; GSPDB:G  
 C:Genetics:  
 A:Gene: CC0771

Query Match 85.3%; Score 29; DB 2; Length 380;  
 Best Local Similarity 80.0%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5  
 Db 161 CHAVC 165

RESULT 65  
 F83010  
 probable oxidoreductase PA5084 [imported] - Pseudomonas aeruginosa (strain PA01)  
 C:Species: Pseudomonas aeruginosa  
 C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
 C:Accession: F83010  
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, N.; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
 A:Reference number: A82950; MUID:20437337; PMID:10984043  
 A:Accession: F83010  
 A:Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-416 <STO>  
A:Cross-references: UNIPROT:Q9HU99; GB:AE004921; GB:AE004091; NID:g9951372; PIDN:AAG0846  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA5084

Query Match 85.3%; Score 29; DB 2; Length 416;  
Best Local Similarity 80.0%; Pred. No. 4.6e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
||| |  
197 CHAFC 201

Db

RESULT 66

AC0809

xanthosine permease [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain xanthosine permease)

C:Species: Salmonella enterica subsp. enterica serovar Typhi  
A:Note: this species has also been called Salmonella typhi  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: AC0809  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R.; Parkhill, J.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AC0809  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-418 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD07653.1; PID:g16503640; GSPDB:GN00176  
C:Genetics:  
A:Gene: STV2657

Query Match 85.3%; Score 29; DB 2; Length 418;  
Best Local Similarity 80.0%; Pred. No. 4.6e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
||| |  
75 CHLVC 79

Db

RESULT 67

E65014

xanthosine permease - Escherichia coli (strain K-12)

C:Species: Escherichia coli  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
C:Accession: E65014  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: E65014  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-418 <BLAT>  
A:Cross-references: UNIPROT:P45562; GB:AE000328; GB:U00096; NID:g2367135; PIDN:AAC75459  
A:Experimental source: strain K-12, substrain MGL655  
C:Genetics:  
A:Gene: xapB

Query Match 85.3%; Score 29; DB 2; Length 418;  
Best Local Similarity 80.0%; Pred. No. 4.6e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
||| |

Db

RESULT 68

T52320

10-deacetyltransferase [imported] - Taxus cuspidata

C:Species: Taxus cuspidata  
C:Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 09-Jul-2004  
C:Accession: T52320  
R:Walker, K.; Croteau, R.  
Proc. Natl. Acad. Sci. U.S.A. 97, 583-587, 2000  
A:Title: Molecular cloning of a 10-deacetyltransferase cDNA from Taxus cuspidata  
A:Reference number: Z26035  
A:Accession: T52320  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-440 <WAL>  
A:Cross-references: UNIPROT:Q9M6E2; EMBL:AF193765; PIDN:AAF27621.1  
C:Genetics:  
A:Gene: DEAT

Query Match 85.3%; Score 29; DB 2; Length 440;  
Best Local Similarity 60.0%; Pred. No. 4.8e+02;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
||| |  
161 CHGIC 165

Db

RESULT 69

T00918

hypothetical protein F21B7.32 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
C:Accession: T00918  
R:Shinn, P.; Euehler, E.; Dewar, K.; Peng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Conologis, A.; Ecker, J.R.  
submitted to the EMBL Data Library, January 1998  
A:Description: Genomic sequence for Arabidopsis thaliana BAC F21B7.  
A:Reference number: Z14208  
A:Accession: T00918  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-461 <SHI>  
A:Cross-references: UNIPROT:Q9LR83; EMBL:AC002560; NID:g2618677; PID:g2809263; GSPDB:GNO019  
C:Genetics:  
A:Gene: ATSP:F21B7.32  
A:Map position: 1

Query Match 85.3%; Score 29; DB 2; Length 461;  
Best Local Similarity 60.0%; Pred. No. 5e+02;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
||| |  
176 CHCIC 180

Db

RESULT 70

T20537

hypothetical protein F07A5.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T20537  
R:Wilkinson, J.  
submitted to the EMBL Data Library, May 1996  
A:Reference number: Z19288  
A:Accession: T20537  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-590 <WIL>  
A:Cross-references: UNIPROT:Q19140; EMBL:Z72506; PIDN:CAA96619.1; GSPDB:GN00019; CESP:F0

A;Experimental source: clone F07A5

C;Genetics:

A;Gene: CESP:F07A5.3

A;Map position: 1

A;Introns: 42/3; 101/2; 151/3; 185/2; 208/3; 240/3; 290/1; 333/2; 370/2; 462/3; 487/2

Query Match 85.3%; Score 29; DB 2; Length 590;

Best Local Similarity 80.0%; Pred. No. 5.9e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5

|||||

Db 389 CHACC 393

RESULT 71

JC7361

folitropin receptor precursor - newt

N;Alternate names: follicle-stimulating hormone receptor

C;Species: Cynops pyrrhogaster (newt)

C;Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 09-Jul-2004

C;Accession: JC7361

R;Nakayama, Y.; Yamamoto, T.; Oba, Y.; Nagahama, Y.; Abe, S.

Biochem. Biophys. Res. Commun. 275, 121-128, 2000

A;Title: Molecular cloning, functional characterization, and gene expression of a follicle-stimulating hormone receptor

A;Reference number: JC7361

A;Contents: Testis

A;Accession: JC7361

A;Molecule type: mRNA

A;Residues: 1-696 <NAK>

A;Cross-references: UNIPROT:Q9DGF5; DBJ:AB005587

C;Comment: This protein, containing seven transmembrane domains and a large glycosylated extracellular domain, is expressed in the testis and thyroid stimulating hormone. This receptor has a common signal transduction pathway with the follicle-stimulating hormone receptor.

C;Genetics:

A;Gene: fish-r

C;Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat h

C;Keywords: disulfide bond; glycolysis; glycoprotein; hormone receptor; testis; transmembrane protein

F;1-17/Domain: signal sequence #status predicted <SIG>

F;18-696/Product: follicle-stimulating hormone receptor #status predicted <MAT>

F;18-359/Domain: extracellular #status predicted <EXT>

F;370-389/Domain: transmembrane #status predicted <TM1>

F;402-424/Domain: transmembrane #status predicted <TM2>

F;447-468/Domain: transmembrane #status predicted <TM3>

F;489-511/Domain: transmembrane #status predicted <TM4>

F;532-553/Domain: transmembrane #status predicted <TM5>

F;577-600/Domain: transmembrane #status predicted <TM6>

F;612-633/Domain: transmembrane #status predicted <TM7>

F;46,190,198,267,292/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;445-520/Disulfide bonds: #status predicted

Query Match 85.3%; Score 29; DB 2; Length 696;

Best Local Similarity 80.0%; Pred. No. 6.7e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5

|||||

Db 18 CHPVC 22

RESULT 72

T20635

hypothetical protein F09B9.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T20635

R;Kershaw, J.

submitted to the EMBL Data Library, June 1995

A;Reference number: Z19303

A;Accession: T20635

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-710 <WIL>

A;Cross-references: UNIPROT:Q19239; EMBL:Z49887; PIDN:CAA90058.1; GSPDB:GN00028; CESP:FO

A;Experimental source: clone F09B9

C;Genetics:

A;Gene: CESP:F09B9.1

A;Map position: X

A;Introns: 82/1; 196/2; 379/1; 626/3; 655/2

C;Superfamily: Caenorhabditis elegans hypothetical protein F09B9.1

Query Match 85.3%; Score 29; DB 2; Length 710;

Best Local Similarity 80.0%; Pred. No. 6.8e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5

|||||

Db 177 CHAYC 181

RESULT 73

T39715

probable transcription regulator, phd finger protein - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C;Accession: T39715

R;Beck, A.; Reinhardt, R.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, September 1998

A;Reference number: Z21872

A;Accession: T39715

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-767 <BEC>

A;Cross-references: UNIPROT:Q74759; EMBL:AL031739; PIDN:CAA21075.1; GSPDB:GN00067; SPDB:4

A;Experimental source: strain 972h-; cosmid c17D11

C;Genetics:

A;Gene: SPDB:SPBC17D11.04c

A;Map position: 2

Query Match 85.3%; Score 29; DB 2; Length 767;

Best Local Similarity 60.0%; Pred. No. 7.2e+02;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5

|||||

Db 270 CHTIC 274

RESULT 74

D96503

protein F9C16.9 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C;Accession: D96503

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;

anssen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, R.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: D96503

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-946 <STO>

A;Cross-references: UNIPROT:Q9LP09; GB:AE005173; NID:g8778679; PIDN:AAF9687.1; GSPDB:GN1

C;Genetics:

A;Gene: F9C16.9

A;Map position: 1

Query Match 85.3%; Score 29; DB 2; Length 946;

Best Local Similarity 80.0%; Pred. No. 8.3e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||  
Db 96 CHVC 100

RESULT 75  
JC4387  
epidermal growth factor receptor homolog precursor - rat  
N;Alternate names: ErbB3 protein; HER3 protein  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 17-Jan-1996 #sequence\_revision 19-Apr-1996 #text\_change 16-Aug-2004  
C;Accession: JC4387  
R;Hellyer, N.J.; Kim, H.H.; Greaves, C.H.; Sierke, S.L.; Koland, J.G.  
Gene 165, 279-284, 1995  
A;Title: Cloning of the rat ErbB3 cDNA and characterization of the recombinant protein.  
A;Reference number: JC4387; MUID:96096535; PMID:8522190  
A;Accession: JC4387  
A;Molecule type: mRNA  
A;Residues: 1-1339 <HEL>  
A;Cross-references: GB:U293339; NID:g915389; PID:g915390  
A;Experimental source: liver  
A;Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue 370.  
C;Comment: This protein is a functional heregulin receptor that transduces signals to the cell.  
C;Genetics:  
A;Gene: ErbB3  
C;Superfamily: protein kinase homology  
C;Keywords: ATP; growth factor receptor; liver; phosphoprotein; transmembrane protein  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-1339/Product: epidermal growth factor homolog #status predicted <WAT>  
F;640-659/Domain: transmembrane #status predicted <TMM>  
F;705-970/Domain: protein kinase homology <KIN>  
F;713-721/Region: protein kinase ATP-binding motif  
F;939, 1051, 1156, 1194, 1196, 1219, 1257, 1259, 1273, 1286, 1325/Binding site: phosphate (Tyr) (C)  
Query Match 85.3%; Score 29; DB 2; Length 1339;  
Best Local Similarity 80.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||  
Db 186 CHEVC 190

RESULT 76  
A36223  
kinase-related transforming protein (erbB3) (EC 2.7.1.-) precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 04-Oct-1991 #sequence\_revision 13-Jan-1993 #text\_change 09-Jul-2004  
C;Accession: A36223; I59164  
R;Kraus, M.H.; Issing, W.; Miki, T.; Popescu, N.C.; Aaronson, S.A.  
Proc. Natl. Acad. Sci. U.S.A. 86, 9193-9197, 1989  
A;Title: Isolation and characterization of ERBB3, a third member of the ERBB/epidermal growth factor receptor gene family.  
A;Reference number: A36223; MUID:90083234; PMID:2687875  
A;Accession: A36223  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1342 <KRA>  
A;Cross-references: UNIPROT:P21860; GB:M29366  
R;Plowman, G.D.; Whitney, G.S.; Neubauer, M.G.; Green, J.M.; McDonald, V.L.; Todaro, G.J.  
Proc. Natl. Acad. Sci. U.S.A. 87, 4905-4909, 1990  
A;Title: Molecular cloning and expression of another epidermal growth factor receptor-related protein.  
A;Reference number: I59164; MUID:9031312; PMID:2164210  
A;Accession: I59164  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-559, 'G', 561-957, 'F', 959-1063, 'G', 1065-1342 <RES>  
A;Cross-references: GB:M34309; NID:g183990; PIDN:AAA35979.1; PID:g306841  
C;Genetics:  
A;Gene: GDB:ERBB3; HER3  
A;Cross-references: GDB:119880; OMIM:190151  
A;Map position: 12q13-12q13  
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

C;Keywords: ATP; phosphotransferase  
F;705-723/Domain: protein kinase ATP-binding motif

Query Match 85.3%; Score 29; DB 2; Length 1342;  
Best Local Similarity 80.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||  
Db 186 CHEVC 190

RESULT 77  
T00209  
MEGF8 protein - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Jan-1999 #sequence\_revision 22-Jan-1999 #text\_change 21-Jul-2000  
C;Accession: T00209  
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.  
Genomics 51, 27-34, 1998  
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs  
A;Reference number: Z14126; MUID:98360089; PMID:9693030  
A;Accession: T00209  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1737 <NAK>  
A;Cross-references: EMBL:AB011541; NID:G3449307; PIDN:BAA32469.1; PID:G3449308  
A;Experimental source: brain; clone HG1392  
C;Genetics:  
A;Gene: MEGF8  
A;Map position: 19q12

Query Match 85.3%; Score 29; DB 2; Length 1737;  
Best Local Similarity 80.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||  
Db 1194 CHAFC 1198

RESULT 78  
T18472  
hypothetical protein C0440c - malaria parasite (Plasmodium falciparum)  
C;Species: Plasmodium falciparum  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T18472  
R;Lawson, D.; Bowman, S.; Barrell, B.  
Submitted to the EMBL Data Library, November 1998  
A;Reference number: Z18937  
A;Accession: T18472  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-2269 <LAW>  
A;Cross-references: UNIPROT:O77360; EMBL:AL008970; NID:e1407852; PID:e1332566; PIDN:CAA1  
C;Genetics:  
A;Gene: C0440c  
A;Map position: 3

Query Match 85.3%; Score 29; DB 2; Length 2269;  
Best Local Similarity 60.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||  
Db 1007 CHGIC 1011

RESULT 79  
T38057  
hypothetical protein SPAC1E11.02 - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: T38057  
R;Skelton, J.; Churcher, C.M.; Barrall, B.G.; Rajandream, M.A.; Wood, V.  
submitted to the EMBL Data Library, August 1997  
A;Reference number: Z21751  
A;Accession: T38057  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-110 <SKE>  
A;Cross-references: UNIPROT:O13886; EMBL:Z98599; PIDN:CAB11249.2; GSPDB:GN00066; SPDB:SP  
A;Experimental source: strain 972H-; cosmid c1E11  
C;Genetics:  
A;Gene: SPDB:SPAC1E11.02  
A;Map position: 1  
A;Introns: 33/3; 43/2; 54/3; 58/2

Query Match 82.4%; Score 28; DB 2; Length 110;  
Best Local Similarity 80.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5  
|||  
DB 55 CHAKC 59

## RESULT 80

T17545

hypotheical protein a55L - Chlorella virus PBCV-1

C;Species: Chlorella virus PBCV-1

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T17545

R;Graves, M.V.; Van Etten, J.L.

submitted to the EMBL Data Library, May 1999

A;Reference number: Z18806

A;Accession: T17545

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-131 &lt;GRA&gt;

A;Cross-references: UNIPROT:Q99390; EMBL:U42580; NID:G4028896; PIDN:AAC96423.1

A;Experimental source: specific host Chlorella strain NC64A

C;Genetics:

A;Gene: a55L

## Query Match

Best Local Similarity 82.4%; Score 28; DB 2; Length 131;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5  
|||  
DB 99 CHHVC 103

## RESULT 81

T23781

hypotheical protein M163.6 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T23781

R;Percy, C.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z19798

A;Accession: T23781

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-157 &lt;WIL&gt;

A;Cross-references: UNIPROT:Q93904; EMBL:Z79603; PIDN:CAB01895.1; GSPDB:GN00028; CESP:M1

A;Experimental source: clone M163

C;Genetics:

A;Gene: CESP:M163.6

A;Map position: X

A;Introns: 64/3; 78/3; 99/3; 109/1; 136/1

## Query Match

Best Local Similarity 82.4%; Score 28; DB 2; Length 157;

Best Local Similarity 80.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CHAVC 5  
|||  
DB 29 CHHVC 33

## RESULT 82

I46204

interferon-alpha - dog

C;Species: Canis lupus familiaris (dog)

C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004

C;Accession: I46204; I46205

R;Himmler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.

J. Interferon Res. 7, 173-183, 1987

A;Title: Structure and expression in Escherichia coli of canine interferon-alpha genes.

A;Reference number: I46204; MUID:87281775; PMID:3039013

A;Accession: I46204

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-187 &lt;HIM&gt;

A;Cross-references: UNIPROT:P81255; GB:M28624; NID:G163973; PIDN:AAA30850.1; PID:G163974

A;Accession: I46205

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-187 &lt;H12&gt;

A;Cross-references: GB:M28625; NID:G163975; PIDN:AAA30851.1; PID:G163976

C;Genetics:

A;Gene: IFN-alpha

C;Superfamily: interferon alpha

## Query Match

Best Local Similarity 82.4%; Score 28; DB 2; Length 187;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
||:|  
DB 16 CHSLC 20

## RESULT 83

I46206

interferon-alpha - dog

C;Species: Canis lupus familiaris (dog)

C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004

C;Accession: I46206

R;Himmler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.

J. Interferon Res. 7, 173-183, 1987

A;Title: Structure and expression in Escherichia coli of canine interferon-alpha genes.

A;Reference number: I46204; MUID:87281775; PMID:3039013

A;Accession: I46206

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-187 &lt;HIN&gt;

A;Cross-references: UNIPROT:O97945; GB:M28626; NID:G163977; PIDN:AAA30852.1; PID:G163978

C;Genetics:

A;Gene: IFN-alpha

C;Superfamily: interferon alpha

## Query Match

Best Local Similarity 82.4%; Score 28; DB 2; Length 187;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
||:|  
DB 16 CHSLC 20

## RESULT 84

AC0359

probable membrane protein YPO2952 [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis

C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
 C;Accession: AC03359  
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Li, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001  
 A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
 A;Reference number: AB0001; MUID:21470413; PMID:11586360  
 A;Accession: AC03359  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-227 <KUR>  
 A;Cross-references: UNIPROT:Q8ZCM9; GB:AL590842; PIDN:CAC92198.1; PID:G15980910; GSPDB:G00041  
 C;Genetics:  
 A;Gene: YPO2952

Query Match 82.4%; Score 28; DB 2; Length 227;  
 Best Local Similarity 60.0%; Pred. No. 4.5e+02;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 |||  
 Db 58 CHQIC 62

RESULT 85  
 T43487  
 hypothetical protein DKFZp434B217.1 - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
 C;Accession: T43487  
 R;Koehler, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, December 1999  
 A;Reference number: Z22514  
 A;Accession: T43487  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-230 <ARA>  
 A;Cross-references: UNIPROT:Q9UF79; EMBL:AL133566  
 A;Experimental source: adult testis; clone DKFZp434B217  
 C;Genetics:  
 A;Note: DKFZp434B217.1  
 C;Superfamily: kexin; subtilisin homology

Query Match 82.4%; Score 28; DB 2; Length 230;  
 Best Local Similarity 80.0%; Pred. No. 4.5e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 |||  
 Db 127 CHASC 131

RESULT 86  
 C44954  
 fumarate reductase (EC 1.3.99.1) iron-sulfur protein - Wolinella succinogenes  
 N;Alternate names: fumarate reductase chain B  
 C;Species: Wolinella succinogenes  
 C;Date: 03-Jun-1993 #sequence\_revision 19-Jul-1996 #text\_change 12-Jul-2004  
 C;Accession: C44954; S10166  
 R;Lauterbach, F.; Koertner, C.; Albracht, S.P.J.; Unden, G.; Kroeger, A. Arch. Microbiol. 154, 386-393, 1990  
 A;Title: The fumarate reductase operon of Wolinella succinogenes. Sequence and expression  
 A;Reference number: A44954; MUID:91058386; PMID:2244791  
 A;Accession: C44954  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-239 <LAU>  
 A;Cross-references: UNIPROT:P17596; GB:X51509; NID:948511; PIDN:CAA35876.1; PID:G48514  
 R;Koertner, C.; Lauterbach, F.; Tripiet, D.; Unden, G.; Kroeger, A. Mol. Microbiol. 4, 855-860, 1990  
 A;Title: Wolinella succinogenes fumarate reductase contains a dihaem cytochrome b.  
 A;Reference number: S10164; MUID:90355847; PMID:2388563

A;Accession: S10166  
 A;Status: preliminary; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-239 <KOE>  
 A;Cross-references: EMBL:X51509; NID:948511; PIDN:CAA35876.1; PID:G48514  
 C;Genetics:  
 A;Gene: frdB  
 A;Complex: part of an enzyme complex containing a heterotrimer (flavoprotein, iron-sulfur)  
 C;Function:  
 A;Description: catalyzes the oxidation of succinate to fumarate and transfers its reduced f the complex together with the iron sulfur subunit  
 C;Superfamily: fumarate reductase/succinate dehydrogenase (ubiquinone), iron-sulfur prot  
 C;Keywords: 2Fe-2S; 3Fe-4S; 4Fe-4S; heterotrimer; iron-sulfur protein; metalloprotein;  
 F;38-78/Domain: ferredoxin [2Fe-2S] homology <PFR1>  
 F;144-226/Domain: ferredoxin [2(4Fe-4S)] homology <PFR2>  
 F;57,62,65,77/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted  
 F;151,154,157,218/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
 F;161,208,214/Binding site: 3Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 82.4%; Score 28; DB 1; Length 239;  
 Best Local Similarity 80.0%; Pred. No. 4.6e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 |||  
 Db 214 CHDVC 218

RESULT 87  
 D86266  
 hypothetical protein F3F19.22 - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C;Accession: D86266  
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, K.; Huizar, L. Nature 408, 816-820, 2000  
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A;Reference number: A86141; MUID:21016719; PMID:11130712  
 A;Accession: D86266  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-260 <STO>  
 A;Cross-references: UNIPROT:Q9SAF3; GB:AE005172; NID:G4850408; PIDN:AAD31078.1; GSPDB:GN  
 C;Genetics:  
 A;Map position: 1  
 C;Superfamily: Arabidopsis thaliana hypothetical protein F7A7.40; RING finger homology

Query Match 82.4%; Score 28; DB 2; Length 260;  
 Best Local Similarity 60.0%; Pred. No. 4.9e+02;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 |||  
 Db 178 CHSMC 182

RESULT 88  
 AG0041  
 L-rhamnose operon transcription activator rhaR [imported] - *Yersinia pestis* (strain CO92)  
 C;Species: *Yersinia pestis*  
 C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
 C;Accession: AG0041  
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Li, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001



A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AG0041

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-290 <R>

A;Cross-references: UNIPROT:Q821Z3; GB:AL590842; PIDN:CAC89194.1; PID:g15978433; GSPDB:G

C;Genetics:

C;Superfamily: hypothetical protein b2382

Query Match 82.4%; Score 28; DB 2; Length 290;

Best Local Similarity 80.0%; Pred. No. 5.3e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 231 CHAKC 235

RESULT 89

JE0174

frizzled protein-2 - human

C;Species: Homo sapiens (man)

C;Date: 03-Jul-1998 #sequence\_revision 10-Jul-1998 #text\_change 09-Jul-2004

C;Accession: JE0174

R;Hu, B.; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Beeley, L.; Brooks, D.

Biochem. Biophys. Res. Commun. 247, 287-293, 1998

A;Title: Tissue restricted expression of two human frzbs in preadipocytes and pancreas.

A;Reference number: JE0174; MUID:98308108; PMID:9642118

A;Accession: JE0174

A;Molecule type: mRNA

A;Residues: 1-295 <HUA>

A;Cross-references: UNIPROT:Q9HAPS

C;Genetics:

A;Map position: 4q

Query Match 82.4%; Score 28; DB 2; Length 295;

Best Local Similarity 80.0%; Pred. No. 5.4e+02;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 114 CHSLC 118

RESULT 90

T22393

hypothetical protein F49A5.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T22393

R;Mortimore, B.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z19560

A;Accession: T22393

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-308 <MIL>

A;Cross-references: UNIPROT:O45530; EMBL:Z81542; PIDN:CAB04415.1; GSPDB:GN00023; CESP:F4

A;Experimental source: clone F49A5

C;Genetics:

A;Gene: CESP:F49A5.4

A;Map position: 5

A;Introns: 46/1; 95/3; 144/1; 187/1

Query Match 82.4%; Score 28; DB 2; Length 308;

Best Local Similarity 80.0%; Pred. No. 5.6e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 297 CHPVC 301

RESULT 91

JC7096

leukotriene B4 receptor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C;Accession: JC7096

R;Toda, A.; Yokomizo, T.; Masuda, K.; Nakao, A.; Izumi, T.; Shimizu, T.

Biochem. Biophys. Res. Commun. 262, 806-812, 1999

A;Title: Cloning and characterization of rat leukotriene B4 receptor.

A;Reference number: JC7096; MUID:99400454; PMID:10471406

A;Accession: JC7096

A;Molecule type: mRNA

A;Residues: 1-351 <TOD>

A;Cross-references: UNIPROT:Q9R0Q2; DBJ:AB025230; NID:G5921091; PIDN:BA84578.1; PID:G5:

C;Genetics:

A;Gene: blt

C;Superfamily: vertebrate rhodopsin

C;Keywords: disulfide bond; glycoprotein; receptor; signal transduction; transmembrane p

Query Match 82.4%; Score 28; DB 2; Length 351;

Best Local Similarity 80.0%; Pred. No. 6.1e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 95 CHYVC 99

RESULT 92

I38429

connexin40 - human

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 13-Aug-1999

C;Accession: I38429

R;Kanter, H.L.; Saffitz, J.E.; Beyer, E.C.

J. Mol. Cell. Cardiol. 26, 861-868, 1994

A;Title: Molecular cloning of two human cardiac gap junction proteins, connexin40 and co

A;Reference number: I38429; MUID:95055780; PMID:7966354

A;Accession: I38429

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-358 <RES>

A;Cross-references: EMBL:U03486; NID:g416327; PIDN:AAA60457.1; PID:g416328

C;Superfamily: gap junction protein

Query Match 82.4%; Score 28; DB 2; Length 358;

Best Local Similarity 80.0%; Pred. No. 6.2e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 61 CHNVC 65

RESULT 93

A49107

alcohol dehydrogenase (EC 1.1.1.1) I - deer mouse

N;Alternate names: alcohol dehydrogenase 1

C;Species: Peromyscus maniculatus (deer mouse)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C;Accession: A49107

R;Zheng, Y.W.; Bey, M.; Liu, H.; Felder, M.R.

J. Biol. Chem. 268, 24933-24939, 1993

A;Title: Molecular basis of the alcohol dehydrogenase-negative deer mouse. Evidence for c

A;Reference number: A49107; MUID:94043358; PMID:8227055

A;Accession: A49107

A;Molecule type: mRNA

A;Residues: 1-375 <ZHE>

A;Cross-references: UNIPROT:P41680; GB:U15703; NID:g416387; PIDN:AAA40591.1; PID:g416388

C;Comment: The class I alcohol dehydrogenases are pyrazole-sensitive and have a high acti

C;Genetics:



A;Gene: Adh-1  
 C;Complex: homodimer (A2 isozyme)  
 C;Function:  
 A;Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes and  
 A;Pathway: alcohol degradation  
 C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology  
 C;Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidoreductase  
 F;2-375/Product: alcohol dehydrogenase alpha #status predicted <MAT>  
 F;32-366/Domains: long-chain alcohol dehydrogenase homology <LADH>  
 F;195-224/Region: beta-alpha-beta NAD nucleotide-binding fold  
 F;2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted  
 F;47,68,175/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted  
 F;98,101,104,112/Binding site: zinc, noncatalytic (Cys) #status predicted

Query Match 82.4%; Score 28; DB 1; Length 375;  
 Best Local Similarity 80.0%; Pred. No. 6.4e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 |||  
 Db 283 CHASC 287

RESULT 94  
 S07825  
 hypothetical protein 2 - fruit fly (Drosophila melanogaster) transposon FB  
 C;Species: Drosophila melanogaster  
 C;Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 09-Jul-2004  
 C;Accession: S07825  
 R;Templeton, N.S.; Potter, S.S.  
 EMBO J. 8, 1887-1894, 1989  
 A;Title: Complete foldback transposable elements encode a novel protein found in Drosophila  
 A;Reference number: S07824; MUID:89356666; PMID:2548860  
 A;Accession: S07825  
 A;Molecule type: DNA  
 A;Residues: 1-403 <TEM>  
 A;Cross-references: UNIPROT:P16320; EMBL:X15469; NID:G7962; PIDN:CAA33497.1; PID:G7964  
 C;Genetics:  
 A;Gene: FlyBase:NOP  
 A;Cross-references: FlyBase:FBgn0002949  
 C;Keywords: nucleus

Query Match 82.4%; Score 28; DB 2; Length 403;  
 Best Local Similarity 60.0%; Pred. No. 6.7e+02;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 |||  
 Db 336 CHRIC 340

RESULT 95  
 S44909  
 ZK686.4 protein - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
 C;Accession: S44909  
 R;Du, Z.  
 submitted to the EMBL Data Library, June 1993  
 A;Description: Sequence of the C. elegans cosmid ZK686.  
 A;Reference number: S44909  
 A;Accession: S44909  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-407 <DUZ>  
 A;Cross-references: UNIPROT:P34670; EMBL:L17337; NID:G304345; PID:G304346  
 C;Genetics:  
 A;Introns: 156/3; 190/1; 212/3; 333/1  
 C;Keywords: DNA binding; nucleus

Query Match 82.4%; Score 28; DB 2; Length 407;  
 Best Local Similarity 80.0%; Pred. No. 6.8e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 |||  
 Db 50 CHPVC 54

# RESULT 96

B36067  
 thyroid hormone receptor alpha-B - African clawed frog

C;Species: Xenopus laevis (African clawed frog)

C;Date: 08-Mar-1991 #sequence\_revision 08-Mar-1991 #text\_change 09-Jul-2004

C;Accession: B36067

R;Yaoita, Y.; Shi, Y.; Brown, D.D.

Proc. Natl. Acad. Sci. U.S.A. 87, 7090-7094, 1990

A;Title: Xenopus laevis alpha and beta thyroid hormone receptors.

A;Reference number: A36067; MUID:90384953; PMID:2402492

A;Accession: B36067

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-418 <YAO>

A;Cross-references: UNIPROT:P18115; GB:W35344; NID:G214831; PIDN:AAA49970.1; PID:G214832

C;Superfamily: thyroid hormone receptor; erba transforming protein homology

C;Keywords: DNA binding; nucleus; thyroid hormone receptor; transcription regulation; z; zi

F;53-335/Domain: erba transforming protein homology <ERBA>

F;61-81/Region: zinc finger

F;99-123/Region: zinc finger

Query Match 82.4%; Score 28; DB 2; Length 418;

Best Local Similarity 80.0%; Pred. No. 6.9e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5

|||  
 Db 388 CHASC 392

# RESULT 97

A55089

vasopressin V3 receptor - human

N;Alternate names: vasopressin receptor V-1B

C;Species: Homo sapiens (man)

C;Date: 18-Nov-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C;Accession: A55089; S51011

R;Sugimoto, T.; Saito, M.; Mochizuki, S.; Watanabe, Y.; Hashimoto, S.; Kawashima, H.

J. Biol. Chem. 269, 27088-27092, 1994

A;Title: Molecular cloning and functional expression of a cDNA encoding the human V-1b v

A;Reference number: A55089; MUID:95014580; PMID:7929452

A;Accession: A55089

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-424 <SUG>

A;Cross-references: UNIPROT:P47901; GB:D31833; NID:G563981; PIDN:BA06621.1; PID:G563982

R;de Keyser, Y.; Auzan, C.; Lenne, P.; Beldjord, C.; Thibonnier, M.; Bertagna, X.; Claus

FEBS Lett. 356, 215-220, 1994

A;Title: Cloning and characterization of the human V3 pituitary vasopressin receptor.

A;Reference number: S51011; MUID:95104418; PMID:7805841

A;Accession: S51011

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-424 <DBK>

A;Cross-references: EMBL:L37112; NID:G791151; PIDN:AAA65687.1; PID:G722622

A;Note: the sequence from Fig. 2A is inconsistent with that from Fig. 1 in having 371-11

C;Superfamily: oxytocin receptor

C;Keywords: transmembrane protein

Query Match 82.4%; Score 28; DB 2; Length 424;

Best Local Similarity 60.0%; Pred. No. 7e+02;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5

|||  
 Db 223 CHRIC 227

```
RESULT 98
T03152
transcription control protein - alcelaphine herpesvirus 1
C;Species: alcelaphine herpesvirus 1
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03152
R;Ensser, A.; Pflanz, R.; Fleckenstein, B.
J. Virol. 71, 6517-6525, 1997
A;Title: Primary structure of the alcelaphine herpesvirus 1 genome.
A;Reference number: Z14840; MUID:97404659; PMID:9261371
A;Accession: T03152
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-436 <ENS>
A;Cross-references: UNIPROT:O36407; EMBL:AF005370; NID:G2337967; PIDN:AAC58104.1; PID:9261371
C;Genetics:
A;Introns: 17/1
C;Superfamily: saimiri herpesvirus 52K immediate-early protein
Query Match 82.4%; Score 28; DB 2; Length 436;
Best Local Similarity 60.0%; Pred. No. 7.1e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CHAVC 5
|||
Db 327 CHIC 331

RESULT 99
adenosylmethionine-8-amino-7-oxononanoate transaminase (EC 2.6.1.62) - Bacillus sphaericus
N;Alternate names: 7,8-diaminononanoate aminotransferase DAPA aminotransferase; adenosyl
C;Species: Bacillus sphaericus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JQ0507
R;Gloeckler, R.; Ohsawa, I.; Speck, D.; Ledoux, C.; Bernard, S.; Zinsius, M.; Villeval,
Gene 87, 63-70, 1990
A;Title: Cloning and characterization of the Bacillus sphaericus genes controlling the B
A;Reference number: JQ0506; MUID:90236299; PMID:2110099
A;Accession: JQ0507
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-455 <GLO>
A;Cross-references: UNIPROT:P22805; GB:M29292; NID:G142587; PIDN:AAB02325.1; PID:G142589
A;Experimental source: strain IFO3525
C;Comment: The enzyme catalyzes the condensation of 8-amino-7-oxononanoate and S-adenosyl
C;Genetics:
A;Gene: biaoA
A;Start codon: GTG
C;Superfamily: beta-alanine-pyruvate transaminase
C;Keywords: aminotransferase; biotin biosynthesis; phosphoprotein; pyridoxal phosphate
F;285/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
Query Match 82.4%; Score 28; DB 1; Length 455;
Best Local Similarity 80.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CHAVC 5
|||
Db 197 CHACQ 201

RESULT 100
S58882
protein kinase Cdelta (EC 2.7.1.1-) [validated] - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S58882; S71846; T41204; T52473
R;Murakami, H.; Okayama, H.
Nature 374, 817-819, 1995
A;Title: A kinase from fission yeast responsible for blocking mitosis in S phase.
A;Reference number: S58882; MUID:95240713; PMID:7723827
```

```
A;Accession: S58882
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-460 <MUR1>
A;Cross-references: UNIPROT:Q09170; EMBL:X85040; NID:G794146
R;Murakami, H.
submitted to the EMBL Data Library, March 1995
A;Reference number: S71846
A;Accession: S71846
A;Molecule type: mRNA
A;Residues: 1-60, 'G', '62-202, 'I', 204-460 <MUR2>
A;Cross-references: EMBL:X85040; NID:G794146; PIDN:CAAS9410.1; PID:G794147
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
submitted to the EMBL Data Library, July 1999
A;Reference number: Z21978
A;Accession: T41204
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Cross-references: EMBL:AL109736; NID:G5701956; PIDN:CAB52158.1; PID:G5701966; GSPDB:GN
A;Experimental source: strain 972h(-); cosmid c18B5
R;Lindsay, H.D.; Griffiths, D.J.F.; Edwards, R.J.; Christensen, P.U.; Murray, J.M.; Omar
Genes Dev. 12, 382-395, 1998
A;Title: S-phase specific activation of Cds1 kinase defines a subpathway of the checkpoint
A;Reference number: Z26084; MUID:98119835; PMID:9450932
A;Accession: T52473
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-202, 'I', 204-237, 'F', 239-460 <LIN>
A;Cross-references: EMBL:AJ222869; NID:G2689196; PIDN:CAAL1019.1; PID:G2689197
C;Genetics:
A;Gene: SPBC1885.11c; cds1
A;Map position: 3
A;Introns: 86/3; 103/1; 113/3; 142/1; 228/3; 298/3; 368/2
C;Function:
A;Description: EC 2.7.1.1-; protein kinase Cdel [validated, MUID:98119835]; is required to
A;Note: Cds1 is phosphorylated and activated by S-phase arrest and activated by DNA dama
C;Superfamily: protein kinase Cdel; kinase interaction domain homology; protein kinase b
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;62-133/Domain: kinase interaction domain homology <KIH>
F;165-433/Domain: protein kinase homology <KIN>
F;173-181/Region: protein kinase ATP-binding motif
Query Match 82.4%; Score 28; DB 2; Length 460;
Best Local Similarity 60.0%; Pred. No. 7.4e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CHAVC 5
|||
Db 234 CHEIC 238

Search completed: July 27, 2005, 00:01:48
Job time : 43 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2005, 23:51:00 ; Search time 173 Seconds  
(without alignments)

14.800 Million cell updates/sec

Title: US-10-632-678-10  
Perfect score: 34  
Sequence: 1 CHAVC 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	114	2 Q9D974	Q9D974 mus musculus
2	34	100.0	170	2 Q91013	Q91013 human cytom
3	34	100.0	170	2 Q6SX57	Q6SX57 human cytom
4	34	100.0	235	2 Q8SBA1	Q8SBA1 oryza sativ
5	34	100.0	235	2 Q7XC69	Q7XC69 oryza sativ
6	34	100.0	238	2 Q9FPE1	Q9FPE1 arabidopsis
7	34	100.0	244	2 Q8L3T0	Q8L3T0 arabidopsis
8	34	100.0	293	2 Q692Q5	Q692Q5 citrus tris
9	34	100.0	293	2 Q692Q6	Q692Q6 citrus tris
10	34	100.0	293	2 Q692Q7	Q692Q7 citrus tris
11	34	100.0	293	2 Q692Q8	Q692Q8 citrus tris
12	34	100.0	293	2 Q692Q9	Q692Q9 citrus tris
13	34	100.0	293	2 Q692R0	Q692R0 citrus tris
14	34	100.0	293	2 Q692R1	Q692R1 citrus tris
15	34	100.0	293	2 Q692R2	Q692R2 citrus tris
16	34	100.0	381	2 Q8T913	Q8T913 drosophila
17	34	100.0	382	2 Q7X8U8	Q7X8U8 oryza sativ
18	34	100.0	400	2 Q769C8	Q769C8 psychrobact
19	34	100.0	400	2 Q9L514	Q9L514 psychrobact
20	34	100.0	424	2 Q9FRE7	Q9FRE7 oryza sativ
21	34	100.0	465	2 Q7QVC3	Q7QVC3 giardia lam
22	34	100.0	537	2 Q9MZU5	Q9MZU5 sus scrofa
23	34	100.0	544	2 Q69T84	Q69T84 oryza sativ
24	34	100.0	660	2 Q7QY47	Q7QY47 giardia lam
25	34	100.0	3107	2 P87587	P87587 citrus tris
26	34	100.0	3115	2 O10467	O10467 citrus tris
27	34	100.0	3115	2 Q9IFX0	Q9IFX0 citrus tris
28	34	100.0	3115	2 Q9WID7	Q9WID7 citrus tris
29	34	100.0	3122	2 Q8B3T9	Q8B3T9 citrus tris
30	34	100.0	3132	2 Q9DTG5	Q9DTG5 citrus tris
31	34	100.0	5636	2 Q9N9M2	Q9N9M2 leishmania

32	33	97.1	75	2	Q74N15	Q74N15 nanoarchaeu
33	33	97.1	168	2	Q6AAV7	Q6AAV7 propionibac
34	33	97.1	198	2	Q8IBP3	Q8IBP3 plasmodium
35	33	97.1	273	2	Q8Y2B0	Q8Y2B0 taistonias
36	33	97.1	383	2	O76856	O76856 dictyosteli
37	33	97.1	397	2	Q993M6	Q993M6 autonomic
38	33	97.1	402	1	VN34_ROTBS	VN34_ROTBS bovine rota
39	33	97.1	402	1	VN34_ROTBS	VN34_ROTBS porcine rot
40	33	97.1	402	2	Q9PY95	Q9PY95 human rotav
41	33	97.1	428	2	Q9MIQ8	Q9MIQ8 arabidopsis
42	33	97.1	665	2	O71159	O71159 kilham rat
43	33	97.1	668	1	VNCS_PAVL3	VNCS_PAVL3 parvovirus
44	33	97.1	672	1	VNCS_MUMIM	VNCS_MUMIM murine minu
45	33	97.1	672	1	VNCS_MUMIV	VNCS_MUMIV murine minu
46	33	97.1	672	1	VNCS_PAVHH	VNCS_PAVHH hamster par
47	33	97.1	672	2	P88899	P88899 kilham rat
48	33	97.1	672	2	Q8JV14	Q8JV14 rat minute
49	33	97.1	672	2	Q8JV16	Q8JV16 rat minute
50	33	97.1	672	2	Q8JV18	Q8JV18 rat minute
51	33	97.1	672	2	Q8JV28	Q8JV28 kilham rat
52	33	97.1	672	2	Q83429	Q83429 mouse parvo
53	33	97.1	721	2	Q84363	Q84363 murine minu
54	33	97.1	721	2	Q84365	Q84365 murine minu
55	33	97.1	815	2	O6ES22	O6ES22 oryza sativ
56	33	97.1	929	2	Q7XDU9	Q7XDU9 oryza sativ
57	33	97.1	1092	2	Q6L4D3	Q6L4D3 oryza sativ
58	31	91.2	64	1	SCX1_MESTA	SCX1_MESTA mesobuthu
59	31	91.2	108	2	Q8D488	Q8D488 vibrio vuln
60	31	91.2	116	2	Q7MPR2	Q7MPR2 vibrio vuln
61	31	91.2	118	2	Q8C3T4	Q8C3T4 mus musculu
62	31	91.2	124	2	Q8QY23	Q8QY23 rana tigrin
63	31	91.2	139	2	Q8TWX8	Q8TWX8 methanopyru
64	31	91.2	168	2	Q91019	Q91019 human cytom
65	31	91.2	168	2	O6SX91	O6SX91 human cytom
66	31	91.2	168	2	O6SX88	O6SX88 human cytom
67	31	91.2	170	2	Q914P6	Q914P6 human cytom
68	31	91.2	170	2	Q914P8	Q914P8 human cytom
69	31	91.2	170	2	Q914P9	Q914P9 human cytom
70	31	91.2	171	1	IR10_HCMVA	IR10_HCMVA human cytom
71	31	91.2	171	2	Q914P7	Q914P7 human cytom
72	31	91.2	171	2	O69029	O69029 human cytom
73	31	91.2	171	2	O6SX75	O6SX75 human cytom
74	31	91.2	171	2	Q6SX66	Q6SX66 human cytom
75	31	91.2	171	2	Q7M6G1	Q7M6G1 human cytom
76	31	91.2	222	2	Q8C2H6	Q8C2H6 mus musculu
77	31	91.2	222	2	Q8C2R3	Q8C2R3 mus musculu
78	31	91.2	230	2	Q8WYK4	Q8WYK4 homo sapien
79	31	91.2	232	2	Q8QNF2	Q8QNF2 ectocarpus
80	31	91.2	251	2	Q9FYL9	Q9FYL9 arabidopsis
81	31	91.2	261	2	Q7MU57	Q7MU57 porphyromon
82	31	91.2	272	2	Q9VDN1	Q9VDN1 drosophila
83	31	91.2	279	2	Q8WYK3	Q8WYK3 homo sapien
84	31	91.2	307	1	TVSY_MOUSE	TVSY_MOUSE mus musculu
85	31	91.2	307	1	TVSY_RAT	TVSY_RAT mus musculu
86	31	91.2	307	2	Q9D0H1	Q9D0H1 mus musculu
87	31	91.2	307	2	Q8VDV6	Q8VDV6 mus musculu
88	31	91.2	310	2	Q8MQS5	Q8MQS5 drosophila
89	31	91.2	312	1	TVSY_HUMAN	TVSY_HUMAN homo sapien
90	31	91.2	318	2	O6P0J5	O6P0J5 brachydanio
91	31	91.2	319	2	Q7ZUI7	Q7ZUI7 brachydanio
92	31	91.2	319	2	Q9DGH5	Q9DGH5 brachydanio
93	31	91.2	373	2	P91501	P91501 caenorhabdi
94	31	91.2	380	2	Q8EED1	Q8EED1 shewanella
95	31	91.2	387	2	Q8XR48	Q8XR48 raletonia s
96	31	91.2	391	2	Q756V7	Q756V7 ashbya goss
97	31	91.2	404	2	Q6DD86	Q6DD86 xenopus lae
98	31	91.2	447	2	Q8XQ02	Q8XQ02 neurospora
99	31	91.2	481	2	Q89GE2	Q89GE2 bradyrhizob
100	31	91.2	502	2	Q7QDB4	Q7QDB4 anopheles g

ALIGNMENTS

```

RESULT 1
Q9D974 ID Q9D974 PRELIMINARY; PRT; 114 AA.
AC Q9D974;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:1700127D06 product:similar to tissue kallikrein (EC
DE 3.4.21.35), submandibular MGK-2.
GN Name=1700127D06Rik;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Akawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

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RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK007298; BAB24941.1; -.
DR HSSP; P00756; ISGF.
DR MEROPS; S01.107; -.
DR MGD; MGI:1924249; 1700127D06Rik.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 114 AA; 13082 MW; CF6C05A967C47546 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 35 CHAVC 39

RESULT 2
Q91013 ID Q91013 PRELIMINARY; PRT; 170 AA.
AC Q91013;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE TRL10.
OS Human cytomegalovirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TB40E, and 36vuek;
RX MEDLINE=21635521; PubMed=11773418;
RA Spaderna S., Blessing H., Bogner E., Britt W., Mach M.;
RT "Identification of glycoprotein gpRL10 as a structural component of
RT human cytomegalovirus.";
RL J. Virol. 76:1450-1460(2002).
DR EMBL; AF432092; AAL27474.1; -.
DR EMBL; AF432086; AAL27468.1; -.
DR Pfam; PF06084; Cytomega_TRL10; 1.
SQ SEQUENCE 170 AA; 18940 MW; B496BE5601E33739 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 59 CHAVC 63

RESULT 3
Q6SX57 ID Q6SX57 PRELIMINARY; PRT; 170 AA.
AC Q6SX57;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE RL10.
OS Human cytomegalovirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.

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OX NCBI_TaxID=10359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3157;
RX PubMed=15105547; DOI=10.1099/vir.0.79888-0;
RA Dolan A., Cunningham C., Hector R.D., Hassan-Walker A.F., Lee L.,
RA Addison C., Dargan D.J., McGeoch D.J., Gatherer D., Emery V.C.,
RA Griffiths P.D., Sinsinger C., McSharry B.P., Wilkinson G.W.,
RA Davison A.J.;
RT "Genetic content of wild-type human cytomegalovirus.";
RL J. Gen. Virol. 85:1301-1312(2004).
DR EMBL; AY446863; AAR31286.1; -.
DR InterPro; IPR009284; Cytomega_TRL10.
DR Pfam; PF06084; Cytomega_TRL10; 1.
SQ SEQUENCE 170 AA; 18942 MW; 8C851AB8E3473D71 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 59 CHAVC 63

RESULT 4
Q8SBA1 PRELIMINARY; PRT; 235 AA.
AC Q8SBA1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein OSJNBa0042H09.16;
GN Name=OSJNBa0042H09.16;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
RA Ganesberg K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
RA Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G.,
RA Varaken S.E., Utkerback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,
RA Salzberg S.L., White O., Fraser C.M.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Buell R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC079874; AAL79784.1; -.
DR Gramene; Q8SBA1; -.
DR InterPro; IPR006461; DUF_A_thal_Cys.
DR Pfam; PF04749; DUF614; 1.
DR TIGRFAMs; TIGR01571; A_thal_Cys_rich; 1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25948 MW; 11D13F750B1046F7 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 113 CHAVC 117

RESULT 5
Q7XC69 PRELIMINARY; PRT; 235 AA.
AC Q7XC69;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)

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DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN ORFNames=OSJNBa0042H09.16;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA The Rice Chromosome 10 Sequencing Consortium;
RT "In-depth view of structure, activity, and evolution of rice
RT chromosome 10.";
RL Science 300:1566-1569(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017119; AAP55005.1; -.
DR Gramene; Q7XC69; -.
DR InterPro; IPR006461; DUF_A_thal_Cys.
DR Pfam; PF04749; DUF614; 1.
DR TIGRFAMs; TIGR01571; A_thal_Cys_rich; 1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25948 MW; 11D13F750B1046F7 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 113 CHAVC 117

RESULT 6
Q9FPE1 PRELIMINARY; PRT; 238 AA.
AC Q9FPE1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein At2g45010 (Fragment).
GN Name=At2g45010;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF327424; AAG42014.1; -.
DR InterPro; IPR006461; DUF_A_thal_Cys.
DR Pfam; PF04749; DUF614; 1.
DR TIGRFAMs; TIGR01571; A_thal_Cys_rich; 1.
KW Hypothetical protein.
FT NON_TER 238
SQ SEQUENCE 238 AA; 26581 MW; B272FAA3846A7FB7 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5

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Db          106 CHAVC 110
|||||
RESULT 7
Q8L3T0      PRELIMINARY;      PRT;      244 AA.
AC Q8L3T0; 2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein At2g45010.
GN Name=At2g45010.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Southwick A., Karlin-Neumann G., Nguyen M., Tripp M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Southwick A., Karlin-Neumann G., Nguyen M., Tripp M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RA "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RA thaliana.";
RA Nature 402:761-768 (1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Lin X.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volkovskiy N., Town C.D., Troughan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RA "Full-length messenger RNA sequences greatly improve genome
RA annotation.";
RA Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).
RN [5]
RP SEQUENCE FROM N.A.
RA Brover V., Troughan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RA Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Heuan V.W., Lee J.M.,
RA Quach H.L., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
RA Yu G., Yuan S., Chen H., Cheuk R., Jenes T., Kim C.J., Nguyen M.,
RA Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,
RA Ecker J.R., Theologis A.;
RA Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY120733; AAM53291.1; -
DR EMBL; AC007659; AAD32834.1; -
DR EMBL; AY087375; AAM64925.1; -
DR EMBL; AK118360; BAC42974.1; -
DR EMBL; BT000360; AAN15679.1; -
DR EMBL; BT000899; AAN41299.1; -
DR PIR; E84885; E84985;
DR InterPro; IPR006461; DUF_A_thal_Cys.
DR Pfam; PF04749; DUF614; 1.
DR TIGRFAMs; TIGR01571; A_thal_Cys_rich; 1.
KW Hypothetical protein.
SQ SEQUENCE 244 AA; 27264 MW; F03B26523376E272 CRC64;
Query Match 100.0%; Score 34; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CHAVC 5
DB 106 CHAVC 110
RESULT 8
Q692Q5      PRELIMINARY;      PRT;      293 AA.
AC Q692Q5; 2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE P349 (Fragment).
OS Citrus tristeza virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Closterovirus.
OX NCBI_TaxID=12162;
RN [1]
RP SEQUENCE FROM N.A.
RA Herrera-Isidron L., Hernandez-Valencia M.C., Sanchez-Briseno V.,
RA Irturrisga-Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R.,
RA Martinez-Soriano J.P.;
RA "Molecular analysis of Citrus tristeza virus isolates from Mexico.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY652915; AAT75285.1; -
FT NON_TER 1
FT NON_TER 293
SQ SEQUENCE 293 AA; 32161 MW; 170A2DC266A948AF CRC64;
Query Match 100.0%; Score 34; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CHAVC 5
DB 118 CHAVC 122
RESULT 9
Q692Q6      PRELIMINARY;      PRT;      293 AA.
AC Q692Q6; 2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE P349 (Fragment).
OS Citrus tristeza virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Closterovirus.
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OX NCBI_TaxID=12162;
RN [1]
RP SEQUENCE FROM N.A.
RA Herrera-Isidron L., Hernandez-Valencia M.C., Sanchez-Briseno V.,
RA Iturriga-Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R.,
RA Martinez-Soriano J.P.;
RA "Molecular analysis of Citrus tristeza virus isolates from Mexico.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY652914; AAT75284.1; -.
FT NON_TER 1
FT NON_TER 293
SQ SEQUENCE 293 AA; 32000 MW; 82B2464AC4EB6348 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 118 CHAVC 122

RESULT 10
Q692Q7 PRELIMINARY; PRT; 293 AA.
AC Q692Q7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE P349 (Fragment).
OS Citrus tristeza virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Closterovirus.
OX NCBI_TaxID=12162;
RN [1]
RP SEQUENCE FROM N.A.
RA Herrera-Isidron L., Hernandez-Valencia M.C., Sanchez-Briseno V.,
RA Iturriga-Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R.,
RA Martinez-Soriano J.P.;
RA "Molecular analysis of Citrus tristeza virus isolates from Mexico.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY652913; AAT75283.1; -.
FT NON_TER 1
FT NON_TER 293
SQ SEQUENCE 293 AA; 32066 MW; 43CCB67B0D6176A9 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 118 CHAVC 122

RESULT 11
Q692Q8 PRELIMINARY; PRT; 293 AA.
AC Q692Q8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE P349 (Fragment).
OS Citrus tristeza virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Closterovirus.
OX NCBI_TaxID=12162;
RN [1]
RP SEQUENCE FROM N.A.
RA Herrera-Isidron L., Hernandez-Valencia M.C., Sanchez-Briseno V.,
RA Iturriga-Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R.,
RA Martinez-Soriano J.P.;
RA "Molecular analysis of Citrus tristeza virus isolates from Mexico.";
RT
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RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY652912; AAT75282.1; -.
FT NON_TER 1
FT NON_TER 293
SQ SEQUENCE 293 AA; 32131 MW; B530226B67053FDE CRC64;

Query Match 100.0%; Score 34; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 118 CHAVC 122

RESULT 12
Q692Q9 PRELIMINARY; PRT; 293 AA.
AC Q692Q9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE P349 (Fragment).
OS Citrus tristeza virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Closterovirus.
OX NCBI_TaxID=12162;
RN [1]
RP SEQUENCE FROM N.A.
RA Herrera-Isidron L., Hernandez-Valencia M.C., Sanchez-Briseno V.,
RA Iturriga-Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R.,
RA Martinez-Soriano J.P.;
RA "Molecular analysis of Citrus tristeza virus isolates from Mexico.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY652911; AAT75281.1; -.
FT NON_TER 1
FT NON_TER 293
SQ SEQUENCE 293 AA; 32746 MW; C85B45D4DFCB7775 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 118 CHAVC 122

RESULT 13
Q692R0 PRELIMINARY; PRT; 293 AA.
AC Q692R0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE P349 (Fragment).
OS Citrus tristeza virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Closterovirus.
OX NCBI_TaxID=12162;
RN [1]
RP SEQUENCE FROM N.A.
RA Herrera-Isidron L., Hernandez-Valencia M.C., Sanchez-Briseno V.,
RA Iturriga-Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R.,
RA Martinez-Soriano J.P.;
RA "Molecular analysis of Citrus tristeza virus isolates from Mexico.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY652910; AAT75280.1; -.
FT NON_TER 1
FT NON_TER 293
SQ SEQUENCE 293 AA; 32074 MW; D21D1D6D2A3D7ECC CRC64;

Query Match 100.0%; Score 34; DB 2; Length 293;
```



Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
|||||  
Db 118 CHAVC 122

## RESULT 14

Q692R1 Q692R1 PRELIMINARY; PRT; 293 AA.  
AC Q692R1;  
DT 25-OCT-2004 (T-EMBLrel. 28, Created)  
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)  
DE P349 (Fragment).  
OS Citrus tristeza virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;  
OC Closterovirus.  
OX NCBI\_TaxID=12162;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Herrera-Isidron L., Hernandez-Valencia M.C., Sanchez-Briseno V.,  
RA Icurtiaga-Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R.,  
RA Martinez-Soriano J.P.;  
RT "Molecular analysis of Citrus tristeza virus isolates from Mexico."  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AV652909; AAT75279.1; -;  
FT NON\_TER 1  
FT NON\_TER 293  
SQ SEQUENCE 293 AA; 32700 MW; C89B45D4DFCB7775 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 293;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
|||||  
Db 118 CHAVC 122

## RESULT 15

Q692R2 Q692R2 PRELIMINARY; PRT; 293 AA.  
AC Q692R2;  
DT 25-OCT-2004 (T-EMBLrel. 28, Created)  
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)  
DE P349 (Fragment).  
OS Citrus tristeza virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;  
OC Closterovirus.  
OX NCBI\_TaxID=12162;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Herrera-Isidron L., Hernandez-Valencia M.C., Sanchez-Briseno V.,  
RA Icurtiaga-Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R.,  
RA Martinez-Soriano J.P.;  
RT "Molecular analysis of Citrus tristeza virus isolates from Mexico."  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AV652908; AAT75278.1; -;  
FT NON\_TER 1  
FT NON\_TER 293  
SQ SEQUENCE 293 AA; 32172 MW; F587251PA4EC4156 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 293;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
|||||  
Db 118 CHAVC 122

## RESULT 16

Q8T9I3 Q8T9I3 PRELIMINARY; PRT; 381 AA.  
AC Q8T9I3; Q9VH34;  
DT 01-JUN-2002 (T-EMBLrel. 21, Created)  
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)  
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)  
DE AT07283p (CG12812-PA).  
GN ORFNames=CG12812;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Dreesen D., Farfan D., Frise E.,  
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,  
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,  
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
RA Celniker S.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
RA Allred J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Chery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Fabros B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusekern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
Science 287:2185-2195 (2000).  
RL [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,  
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,



RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila  
melanogaster euchromatic genome sequence.";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,  
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
Ashburner M., Celniker S.E.;  
RA "The transposable elements of the Drosophila melanogaster euchromatin:  
a genomics perspective.";  
RT a Genomics perspective.";  
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,  
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
Lewis S.E.;  
RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
systematic review.";  
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
RN [6]  
RP SEQUENCE FROM N.A.  
RX FlyBase;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RX FlyBase;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY075174; AAL68044.1; -;  
DR EMBL; AE003685; AAF54486.2; -;  
DR IntAct; Q8T913; -;  
DR FlyBase; FBgn0037781; CG12812.  
SQ SEQUENCE 381 AA; 43725 MW; 012595FB8830BC9C CRC64;

Query Match 100.0%; Score 34; DB 2; Length 381;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||  
Db 338 CHAVC 342

RESULT 17  
Q7X8U8  
ID Q7X8U8 PRELIMINARY; PRT; 382 AA.  
AC Q7X8U8;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE OSJNB0026E15.3 protein.  
GN Name=OSJNB0026E15.3;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=12447439; DOI=10.1038/nature01183;  
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,  
Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,  
Weng Q., Zhang L., Lu Y., Wu J., Lu Y., Zhang L.S., Yu Z., Fan D.,  
Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,  
Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,  
Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,  
Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang W.,

RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,  
Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,  
Han B.;  
RT "Sequence and analysis of rice chromosome 4.";  
RL Nature 420:316-320(2002).  
DR EMBL; AL607008; CAE03685.2; -;  
DR Gramene; Q7X8U8; -;  
DR InterPro; IPR001810; F-box.  
DR InterPro; IPR006527; F\_box\_assoc.1.  
DR InterPro; IPR011043; Gal\_oxid\_central.  
DR Pfam; PF00646; F-box; 1.  
DR SMART; SM00256; FBOX; 1.  
DR TIGRFAMs; TIGR01640; F\_box\_assoc.1; 1.  
DR PROSITE; PS0181; FBOX; 1.  
SQ SEQUENCE 382 AA; 42864 MW; CF7B92144C7C8E2D CRC64;

Query Match 100.0%; Score 34; DB 2; Length 382;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||  
Db 36 CHAVC 40

RESULT 18  
Q769C8  
ID Q769C8 PRELIMINARY; PRT; 400 AA.  
AC Q769C8;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cold-active esterase.  
GN Name=Psy8at;  
OS Psychrobacter sp. Ant300.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Moraxellaceae; Psychrobacter.  
OX NCBI\_TaxID=235460;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Ant300;  
RA Kulakova L., Galkin A., Nakayama T., Nishino T., Esaki N.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB12812; BAD06009.1; -;  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR002168; Lipolytic enzyme.  
DR InterPro; IPR006025; Pept\_M\_zn\_BS.  
DR InterPro; IPR000379; Ser-estrase.  
DR PROSITE; PS01173; LIPASE\_GDXG\_HIS; 1.  
DR PROSITE; PS01142; ZINC\_PROTEASE; UNKNOWN 1.  
SQ SEQUENCE 400 AA; 43683 MW; 108D59146AB86FDB CRC64;

Query Match 100.0%; Score 34; DB 2; Length 400;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||  
Db 158 CHAVC 162

RESULT 19  
Q9L514  
ID Q9L514 PRELIMINARY; PRT; 400 AA.  
AC Q9L514;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Lipase.  
GN Name=lip;  
OS Psychrobacter sp. (strain Stl).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

```

OC Moraxellaceae; Psychrobacter.
OX NCBI_TaxID=125076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=St1;
RA Kulakova L., Galkin A., Kurihara T., Yoshimura T., Esaki N.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF260707; AAF70342.1; -. F-Box.
DR GO; GO:0016787; F-hydrolase activity; IEA.
DR GO; GO:0008152; P-metabolism; IEA.
DR InterPro; IPR002168; Lipolytic enzyme.
DR InterPro; IPR006025; Pept M.Zn.BS.
DR InterPro; IPR003379; Ser esters.
DR PROSITE; PS01173; LIPASE_GDXG_HTS; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 400 AA; 43683 MW; 1D8D59146ABE6FDB CRC64;

Query Match 100.0%; Score 34; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 158 CHAVC 162

RESULT 20
Q9FRE7
ID Q9FRE7 PRELIMINARY; PRT; 424 AA.
AC Q9FRE7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein OSUNBa0013M12.13;
GN Name=OSUNBa0013M12.13;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan O., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
RA Ziesmann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Buell R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC082644; AAG46124.1; -.
DR Gramene; Q9FRE7; -.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
KW Hypothetical protein.
SQ SEQUENCE 424 AA; 46722 MW; 19B4CB09CF41F02 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 424;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 39 CHAVC 43

RESULT 21
Q7QVC3
ID Q7QVC3 PRELIMINARY; PRT; 465 AA.
AC Q7QVC3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)

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DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP_542_47587_46190.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RL "Draft sequence of the Giardia lamblia genome.";
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAC801000082; EAA39016.1; -.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006058; 2Fe2S fd_BS.
DR InterPro; IPR001450; 4Fe4S-ferredoxin.
DR InterPro; IPR009030; Grow_Fac_recept.
DR PRINTS; PR00353; 4FE4SFRDOXIN.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; UNKNOWN 1.
SQ SEQUENCE 465 AA; 48977 MW; 83D00A8A5357D7DC CRC64;

Query Match 100.0%; Score 34; DB 2; Length 465;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 75 CHAVC 79

RESULT 22
Q9MZU5
ID Q9MZU5 PRELIMINARY; PRT; 537 AA.
AC Q9MZU5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Intercellular adhesion molecule-1 precursor.
GN Name=ICAM-1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=domestic breed; TISSUE=Aorta;
RA Stocker C., Sugars K., Yarwood H., Delikouras A., Dorling A.,
RA Lechler R., Landis C., Morley B., Haskard D.;
RT "Cloning of porcine ICAM-1 and characterization of ITS induction on
RT endothelial cells by cytokines.";
RL J. Immunol. 0:0-0(1999)
DR EMBL; AF156712; AAF80287.1; -.
DR HSPB; P05362; IICL.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016337; P:cell-cell adhesion; IEA.
DR InterPro; IPR003988; ICAM.
DR InterPro; IPR003987; ICAM_VCAM-1.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF03921; ICAM_N; 1.
DR PRINTS; PR01473; ICAM.
DR PRINTS; PR01472; ICAMVCAM1.
DR SMART; SM00409; IG; 3.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Signal.
FT SIGNAL.
FT CHAIN 1 30 Potential.
FT CHAIN 31 537 intercellular adhesion molecule-1.

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SQ SEQUENCE 537 AA; 58430 MW; 47DA0F0F3C75CD54 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 537;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 Db 96 CHAVC 100

RESULT 23

Q69T84 PRELIMINARY; PRT; 544 AA.

AC Q69T84;  
 DT 25-OCT-2004 (TReMBLrel. 28, Created)  
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
 DE Putative P450.

GN Name=P0652D10.24;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OC NCBI\_TaxID=39947;  
 RN [1]

RP SEQUENCE FROM N.A.

RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC clone:P0652D10.";  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Belongs to the cytochrome P450 family.

DR EMBL: AP004757; BAD33240.1; -  
 DR GO: 0004497; P:monooxygenase activity; IEA.  
 DR GO: 0006118; P:electron transport; IEA.  
 DR InterPro: IPR001128; Cytochrome\_P450.  
 DR InterPro: IPR002401; EP4501.  
 DR Pfam: PF00067; P450\_1.  
 DR PRINTS: PRO0463; EP4501.  
 DR PRINTS: PRO0385; P450.  
 DR PROSITE: PS00059; ADH\_ZINC; UNKNOWN\_1.  
 DR PROSITE: PS00086; CYTOCHROME\_P450; I.  
 KW Heme; Monooxygenase; Oxidoreductase.  
 SQ SEQUENCE 544 AA; 61150 MW; 0BF7A97974D0F5E1 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 544;  
 Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 Db 221 CHAVC 225

RESULT 24

Q70Y47 PRELIMINARY; PRT; 660 AA.

AC Q70Y47;  
 DT 01-MAR-2004 (TReMBLrel. 26, Created)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE GLP\_572\_62459\_60477.  
 OS Giardia lamblia ATCC 58003.  
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.  
 OC NCBI\_TaxID=184922;  
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=WB C6;  
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,  
 RA Olsen G.J., Sogin M.L.;  
 RT "Draft sequence of the Giardia lamblia genome.";  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

CC EMBL: AACB01000053; EAA40025.1; -  
 CC GO: 0005489; P:electron transporter activity; IEA.  
 CC GO: 0005506; P:iron ion binding; IEA.  
 CC GO: 0006118; P:electron transport; IEA.  
 CC InterPro: IPR006058; 2Fe2S fd BS.  
 CC InterPro: IPR001450; 4Fe4S ferredoxin.  
 CC InterPro: IPR003345; CytC heme BS.  
 CC InterPro: IPR005127; Giardia VSP.  
 CC InterPro: IPR009030; Grow\_fac\_recept.  
 CC Pfam: PF03302; VSP; 1.  
 CC PRINTS: PRO0353; 4FE4SFRDOXIN.  
 CC PROSITE: PS00197; 2FE2S FERREDOXIN; UNKNOWN\_1.  
 CC PROSITE: PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
 SQ SEQUENCE 660 AA; 66878 MW; 9AC79667499ED91B CRC64;

Query Match 100.0%; Score 34; DB 2; Length 660;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02; Mismatches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 Db 282 CHAVC 286

RESULT 25

P87587 PRELIMINARY; PRT; 3107 AA.

AC P87587;  
 DT 01-MAY-1997 (TReMBLrel. 03, Created)  
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE P346.  
 OS Citrus tristeza virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;  
 OC Closterovirus.  
 OC NCBI\_TaxID=12162;  
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=vt;  
 RX MEDLINE=96406950; PubMed=8811037;  
 RA Mawassi M., Mietkiewska E., Gofman R., Yang G., Bar-Joseph M.;  
 RT "Unusual sequence relationships between two isolates of citrus tristeza virus.";  
 RL J. Gen. Virol. 77:2359-2364(1996).

DR EMBL: U56902; AAB38755.1; -  
 DR GO: 00008174; P:RNA methyltransferase activity; IEA.  
 DR GO: 0003723; P:RNA binding; IEA.  
 DR GO: 0003724; P:RNA helicase activity; IEA.  
 DR GO: 0003968; P:RNA-directed RNA polymerase activity; IEA.  
 DR GO: 0006396; P:RNA processing; IEA.  
 DR GO: 0019079; P:viral genome replication; IEA.  
 DR InterPro: IPR008749; Peptidase\_C42.  
 DR InterPro: IPR000606; Viral\_helicase1.  
 DR InterPro: IPR002588; V\_methyltrans.  
 DR Pfam: PF05533; Peptidase\_C42; 2.  
 DR Pfam: PF01443; Viral\_helicase1; 1.  
 DR Pfam: PF01660; Vmethyltransf; 1.  
 SQ SEQUENCE 3107 AA; 346659 MW; 02B748P693BE89CB CRC64;

Query Match 100.0%; Score 34; DB 2; Length 3107;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03; Mismatches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
 Db 594 CHAVC 598

RESULT 26

O10467

ID O10467 PRELIMINARY; PRT; 3115 AA.  
 AC O10467;  
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE 347-kDa polyprotein.  
 OS Citrus tristeza virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;  
 OC Closterovirus.  
 OX NCBI\_TaxID=12162;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SY568;  
 RX MEDLINE=20007030; PubMed=10541017; DOI=10.1023/A:1008127224147;  
 RA Yang Z.N., Mathews D.M., Dodds J.A., Mirkov T.E.;  
 RT "Molecular characterization of an isolate of citrus tristeza virus  
 RT that causes severe symptoms in sweet orange.";  
 RL Virus Genes 19:131-142(1999).  
 DR EMBL; AF001623; AAB57702.1; -.  
 DR GO; GO:0008174; F:RNA methyltransferase activity; IEA.  
 DR GO; GO:0003723; F:RNA binding; IEA.  
 DR GO; GO:0003724; F:RNA helicase activity; IEA.  
 DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.  
 DR GO; GO:0006396; P:RNA processing; IEA.  
 DR GO; GO:0019079; P:viral genome replication; IEA.  
 DR InterPro; IPR008749; Peptidase C42.  
 DR InterPro; IPR000606; Viral helicase.  
 DR InterPro; IPR002588; V\_methyltrans.  
 DR Pfam; PF05533; Peptidase C42; 2.  
 DR Pfam; PF01443; Viral helicase1; 1.  
 DR Pfam; PF01660; Vmethyltransf; 1.  
 KW Polyprotein.  
 SQ SEQUENCE 3115 AA; 347072 MW; B406EAFB38E73F9 CRC64;  
  
 Query Match 100.0%; Score 34; DB 2; Length 3115;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 CHAVC 5  
 DB 600 CHAVC 604  
  
 RESULT 27  
 ID Q9IFX0 PRELIMINARY; PRT; 3115 AA.  
 AC Q9IFX0;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE P349 protein.  
 OS Citrus tristeza virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;  
 OC Closterovirus.  
 OX NCBI\_TaxID=12162;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=730;  
 RX MEDLINE=20347348; PubMed=10888625;  
 RA DOI=10.1128/JVI.74.15.6856-6865.2000;  
 RA Albiach-Marti M.R., Mawassi M., Gowda S., Satynaravana T., Hilf M.E.,  
 RA Shanker S., Almira E.C., Vives M.C., Lopez C., Guerri J., Flores R.,  
 RA Moreno P., Garnsey S.M., Dawson W.O.;  
 RT "Sequences of citrus tristeza virus separated in time and space are  
 RT essentially identical.";  
 RL J. Virol. 74:6856-6865(2000).  
 DR EMBL; AF260651; AAF70348.1; -.  
 DR GO; GO:0008174; F:RNA methyltransferase activity; IEA.  
 DR GO; GO:0003723; F:RNA binding; IEA.  
 DR GO; GO:0003724; F:RNA helicase activity; IEA.  
 DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.  
 DR GO; GO:0006396; P:RNA processing; IEA.  
 DR GO; GO:0019079; P:viral genome replication; IEA.

DR InterPro; IPR008749; Peptidase C42.  
 DR InterPro; IPR000606; Viral helicase1.  
 DR Pfam; PF05533; Peptidase C42; 2.  
 DR Pfam; PF01443; Viral helicase1; 1.  
 DR Pfam; PF01660; Vmethyltransf; 1.  
 SQ SEQUENCE 3115 AA; 346874 MW; 6B97F494ED25AD63 CRC64;  
  
 Query Match 100.0%; Score 34; DB 2; Length 3115;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 CHAVC 5  
 DB 600 CHAVC 604  
  
 RESULT 28  
 ID Q9WID7 PRELIMINARY; PRT; 3115 AA.  
 AC Q9WID7;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE P349 protein.  
 OS Citrus tristeza virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;  
 OC Closterovirus.  
 OX NCBI\_TaxID=12162;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99190444; PubMed=10092023;  
 RA Vives M.C., Rubio L., Lopez C., Navas-Castillo J., Albiach-Marti M.R.,  
 RA Dawson W.O., Guerri J., Flores R., Moreno P.;  
 RT "The complete genome sequence of the major component of a mild citrus  
 RT tristeza virus isolate.";  
 RL J. Gen. Virol. 80:811-816(1999).  
 DR EMBL; Y18420; CAA77161.1; -.  
 DR GO; GO:0008174; F:RNA methyltransferase activity; IEA.  
 DR GO; GO:0003723; F:RNA binding; IEA.  
 DR GO; GO:0003724; F:RNA helicase activity; IEA.  
 DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.  
 DR GO; GO:0006396; P:RNA processing; IEA.  
 DR GO; GO:0019079; P:viral genome replication; IEA.  
 DR InterPro; IPR008749; Peptidase C42.  
 DR InterPro; IPR000606; Viral helicase1.  
 DR InterPro; IPR002588; V\_methyltrans.  
 DR Pfam; PF05533; Peptidase C42; 2.  
 DR Pfam; PF01443; Viral helicase1; 1.  
 DR Pfam; PF01660; Vmethyltransf; 1.  
 SQ SEQUENCE 3115 AA; 346982 MW; 3EEA612F605D5045 CRC64;  
  
 Query Match 100.0%; Score 34; DB 2; Length 3115;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 CHAVC 5  
 DB 600 CHAVC 604  
  
 RESULT 29  
 ID Q8BJT9 PRELIMINARY; PRT; 3122 AA.  
 AC Q8BJT9;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Polyprotein p349.  
 OS Citrus tristeza virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;  
 OC Closterovirus.  
 OX NCBI\_TaxID=12162;

RP SEQUENCE FROM N.A.  
RX MEDLINE=99307427; PubMed=10377432; DOI=10.1073/pnas.96.13.7433;  
RA Satyanarayana T., Gowda S., Boyko V.P., Albiach-Marti M.R.,  
RA Nawasli M., Navas-Castillo J., Karasev A.V., Dolja V., Hilf M.E.,  
RA Lewandowski D.J., Moreno P., Bar-Joseph M., Garnsey S.M., Dawson W.O.;  
RT "An engineered closterovirus RNA replicon and analysis of heterologous  
terminal sequences for replication.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:7433-7438 (1999).  
[2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22836522; PubMed=12954215; DOI=10.1016/S0042-6822(03)00387-8;  
RA Satyanarayana T., Gowda S., Ayllon M.A., Dawson W.O.;  
RT "Frameshift mutations in infectious cDNA clones of Citrus tristeza  
virus: a strategy to minimize the toxicity of viral sequences to  
Escherichia coli.";  
RL Virology 313:481-491 (2003).  
DR EMBL; AY170468; AA012715.1; -  
DR GO; GO:0008174; F:RNA methyltransferase activity; IEA.  
DR GO; GO:0003723; F:RNA binding; IEA.  
DR GO; GO:0003724; F:RNA helicase activity; IEA.  
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.  
DR GO; GO:0006396; F:RNA processing; IEA.  
DR GO; GO:0019079; F:viral genome replication; IEA.  
DR InterPro; IPR008749; Peptidase C42.  
DR InterPro; IPR006066; Viral helicase.  
DR Pfam; PF05533; Peptidase C42; 2.  
DR Pfam; PF01443; Viral\_helicase1; 1.  
DR Pfam; PF01660; Vmethyltransf; 1.  
KW Polyprotein.  
SQ SEQUENCE 3122 AA; 348272 MW; D7084307FF0ED355 CRC64;  
  
Query Match 100.0%; Score 34; DB 2; Length 3122;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CHAVC 5  
Db 601 CHAVC 605  
  
RESULT 30  
Q9DTG5  
ID Q9DTG5 PRELIMINARY; PRT; 3132 AA.  
AC Q9DTG5:  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE 349-kDa polyprotein.  
GN Name=p349;  
OS Citrus tristeza virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;  
OC Closterovirus.  
OX NCBI\_TaxID=121162;  
RP SEQUENCE FROM N.A.  
RC STRAIN=seedling yellows strain;  
RA Suatika G., Natsuaki T., Kano T., Ieki H., Okuda S.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB046398; BAB18522.1; -  
DR GO; GO:0008174; F:RNA binding; IEA.  
DR GO; GO:0003723; F:RNA methyltransferase activity; IEA.  
DR GO; GO:0003724; F:RNA helicase activity; IEA.  
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.  
DR GO; GO:0006396; F:RNA processing; IEA.  
DR GO; GO:0019079; F:viral genome replication; IEA.  
DR InterPro; IPR008749; Peptidase C42.  
DR InterPro; IPR006066; Viral helicase.  
DR Pfam; PF05533; Peptidase C42; 2.  
DR Pfam; PF01443; Viral\_helicase1; 1.  
DR Pfam; PF01660; Vmethyltransf; 1.

KW Polyprotein.  
SQ SEQUENCE 3132 AA; 349380 MW; 4A7A1DDDD7DEC9463 CRC64;  
  
Query Match 100.0%; Score 34; DB 2; Length 3132;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CHAVC 5  
Db 600 CHAVC 604  
  
RESULT 31  
Q9N9M2  
ID Q9N9M2 PRELIMINARY; PRT; 5636 AA.  
AC Q9N9M2:  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Possible RJS/HERC2-like protein (possible herc2-related protein).  
GN Name=L3665.04; Synonyms=P265.01;  
OS Leishmania major.  
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
OX NCBI\_TaxID=5664;  
RP SEQUENCE FROM N.A.  
RC STRAIN=Friedlin;  
RX MEDLINE=98146435; PubMed=9477341;  
RA Ivans A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,  
RA Smith D.F.;  
RT "A physical map of the Leishmania major Friedlin genome.";  
RL Genome Res. 8:135-145 (1998).  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Friedlin;  
RA Aert R., Robben J., Weltjens I., Grymonprez B., Volckaert G.,  
RA Ivans A.C., Quail M., Rajandream M.A., Barrell B.G.;  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
[3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Friedlin;  
RA Robben J., Grymonprez B., Weltjens I., Aert R., Volckaert G.,  
RA Ivans A.C., Quail M., Rajandream M.A., Barrell B.G.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL359775; CAB95249.2; -  
DR EMBL; AL359716; CAD19412.1; -  
DR GO; GO:0005622; C:intracellular; IEA.  
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.  
DR GO; GO:0006512; F:ubiquitin cycle; IEA.  
DR InterPro; IPR000569; HECT.  
DR InterPro; IPR001400; Somatotropin.  
DR Pfam; PF00622; SPRY; 2.  
DR SMART; SM00119; HECTC; 1.  
DR PROSITE; PS00237; HECT; 1.  
DR PROSITE; PS00338; SOMATOTROPIN 2; UNKNOWN 1.  
SQ SEQUENCE 5636 AA; 593224 MW; 84D6DDDD4B0A5E694 CRC64;  
  
Query Match 100.0%; Score 34; DB 2; Length 5636;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CHAVC 5  
Db 1030 CHAVC 1034  
  
RESULT 32  
Q74N15  
ID Q74N15 PRELIMINARY; PRT; 75 AA.  
AC Q74N15:  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE NEQ373
GN OrderedLocusNames=NEQ373;
OS Nanoarchaeum equitans.
OC Archaea; Nanoarchaeota; Nanoarchaeum.
OX NCBI_TaxID=160232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Kin4-M;
RX MEDLINE=22946215; PubMed=14566062; DOI=10.1073/pnas.1735403100;
RA Waters E., Hohn M.J., Ahel I., Graham D.E., Adams M.D., Barnstead M.,
RA Beeson K.Y., Bibbs L., Bolanos R., Keller M., Kretz K., Lin X.,
RA Mathur E., Ni J., Podar M., Richardson T., Sutton G.G., Simon M.,
RA Seell D., Stetter K.O., Short J.M., Noorderwier M.;
RT "The genome of Nanoarchaeum equitans: insights into early archaeal
RT evolution and derived parasitism.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:12984-12988 (2003).
DR EMBL; AE017199; AAC39222.1; -.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR Pfam; PF00037; Fer4; 1.
DR PRINTS; PR00353; 4FE4SFRDOXIN.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN 1.
KW 4Fe-4S; Complete proteome; Iron; iron-sulfur; Metal-binding.
SQ SEQUENCE 75 AA; 7981 MW; B65608374A5CE9 CRC64;

Query Match 97.1%; Score 33; DB 2; Length 75;
Best Local Similarity 80.0%; Pred. No. 72;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 17 CHAIC 21

RESULT 33
Q6AAV7 PRELIMINARY; PRT; 168 AA.
ID Q6AAV7
AC Q6AAV7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (EC
DE 4.6.1.12).
GN OrderedLocusNames=PPA0354;
OS Propionibacterium acnes.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Propionibacterineae; Propionibacteriaceae; Propionibacterium.
OX NCBI_TaxID=1747;
RN [1]
RP SEQUENCE FROM N.A.
RC Science 305:671-673 (2004).
RX STRAIN=KPA171202 / DSM 16379;
RX PubMed=15286373; DOI=10.1126/science.1100330;
RA Brueggemann H., Henne A., Hostet F., Liesegang H., Wierer A.,
RA Strittmatter A., Hujer S., Duerre P., Gottschalk G.;
RT "The complete genome sequence of Propionibacterium acnes, a commensal
RT of human skin.";
RL Science 305:671-673 (2004).
DR EMBL; AE017283; AAT82109.1; -.
DR GO; GO:0008685; F:2-C-methyl-D-erythritol 2,4-cyclodiphosphat...; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0016114; P:terpenoid biosynthesis; IEA.
DR InterPro; IPR010925; MECDDP synth.
DR InterPro; IPR003526; YgbB_synth.
DR Pfam; PF02542; YgbB; 1.
DR PIRSF; PIRSF005911; MECDDP synth; 1.
DR TIGRFAMS; TIGR00151; ispF; 1.
DR PROSITE; PS01350; ISP; 1.
KW Complete proteome; Lyase.
SQ SEQUENCE 168 AA; 16829 MW; DF6C56D1DD903042 CRC64;

Query Match 97.1%; Score 33; DB 2; Length 198;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 113 CHAIC 117

RESULT 35
Q8Y2B0 PRELIMINARY; PRT; 273 AA.
ID Q8Y2B0
AC Q8Y2B0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein RSC0426.
GN Name=RSC03995; OrderedLocusNames=RS0426;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RX STRAIN=CM11000;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billat A., Brottier P., Camus J.C., Cartolico L.,
RA Chandler M., Cholsne N., Claudel-Renard C., Cunac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Sigulier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502 (2002).
DR EMBL; AL646059; CAD13954.1; -.
KW Complete proteome.
SQ SEQUENCE 273 AA; 28364 MW; 2B4AF9D2BA1BA14A CRC64;

Query Match 97.1%; Score 33; DB 2; Length 168;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 45 CHAIC 49

RESULT 34
Q8IBP3 PRELIMINARY; PRT; 198 AA.
ID Q8IBP3
AC Q8IBP3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein MAL7P1.110.
GN Name=MAL7P1.110;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
RA Quail M., Barrell B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL844506; CAD50956.1; -.
DR HSSP; Q57679; 1B78.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR002637; Hamlp_like.
DR Pfam; PF01725; Hamlp; 1.
KW Hypothetical protein.
SQ SEQUENCE 198 AA; 23080 MW; CE0AA63F011B3D3E CRC64;

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Thu Jul 28 07:51:38 2005

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Query Match          97.1%; Score 33; DB 2; Length 273;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAUC 5
Db 94 CHAIC 98

RESULT 36
O76856 PRELIMINARY; PRT; 383 AA.
AC O76856;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Precocathepsin D precursor (EC 3.4.23.5).
GN Name=ctsd;
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=Ax2, and Ax-2;
RX MEDLINE=99454799; PubMed=10523518;
RA Journet A.M., Chapel A., Jehan S., Adessi C., Freeze H., Klein G.,
RA Garin J.;
RT "Characterization of Dictyostelium discoideum cathepsin D. Molecular
RT cloning, gene disruption, endo-lysosomal localization and sugar
RT modifications.";
RL J. Cell Sci. 112:3833-3843(1999).
CC -1- SIMILARITY: Belongs to peptidase family A1.
DR EMBL; Y16962; CAA76563.1; --
DR EMBL; AJ243946; CAB57223.1; --
DR HSSP; P00794; 4CMS.
DR DictyBase; DDB0215012; ctsd.
DR GO; GO:0004192; F:cathepsin D activity; IEA.
DR GO; GO:0004194; F:pepsin A activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001461; Peptidase A1.
DR InterPro; IPR009007; Pept_Aspartic.
DR InterPro; IPR001969; Pept_Asp_AS.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
KW Aspartyl protease; Hydrolase; Protease; Signal.
FT SIGNAL 18 Potential.
FT CHAIN 49 383 cathepsin D.
SQ SEQUENCE 383 AA; 41120 MW; CC8DE423AEAI280 CRC64;

Query Match          97.1%; Score 33; DB 2; Length 383;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAUC 5
Db 263 CHAIC 267

RESULT 37
Q993M6 PRELIMINARY; PRT; 397 AA.
AC Q993M6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural protein 1 (Fragment).
GN Name=NS1;
OS Autonomus rat parvovirus RV-Y.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX NCBI_TaxID=155025;
RN [1];
RP SEQUENCE FROM N.A.
```

```
RC STRAIN=Yale;
RX MEDLINE=21102993; PubMed=11172095;
RA Ball-Goodrich L.J., Johnson S., Jacoby R.;
RT "Divergent replication kinetics of two phenotypically different
RT parvoviruses of rats.";
RL J. Gen. Virol. 82:537-546(2001).
DR EMBL; AF317513; AAK27438.1; --
DR GO; GO:0019012; C:virion; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
DR InterPro; IPR001257; Parvo NS1.
DR Pfam; PF01057; Parvo NS1; 1.
KW Nonstructural protein.
FT NON_TER 1
SQ SEQUENCE 397 AA; 43959 MW; D62052E4767366BB CRC64;

Query Match          97.1%; Score 33; DB 2; Length 397;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAUC 5
Db 103 CHAIC 107

RESULT 38
VN34 ROTBS STANDARD; PRT; 402 AA.
AC P34717;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Nonstructural RNA-binding protein 34 (NS34) (NCVp4).
GN Name=S6;
OS Bovine rotavirus (group C / strain Shintoku).
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=33723;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=93275758; PubMed=8389040;
RA Jiang B., Teunemaitau H., Gentsch J.R., Saif L.J., Glass R.I.;
RT "Nucleotide sequences of genes 6 and 10 of a bovine group C
RT rotavirus.";
RL Nucleic Acids Res. 21:2250-2250(1993).
CC -1- SIMILARITY: Contains 1 DBEM (double-stranded RNA-binding) domain.
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CC -----
DR EMBL; L12390; --; NOT_ANNOTATED_CDS.
DR PIR; S35639; S35639.
DR InterPro; IPR001159; DS_RBD.
DR InterPro; IPR002873; Rota_NSP3.
DR Pfam; PF00035; darm; 1.
DR Pfam; PF01665; Rota_NSP3; 1.
DR SMART; SM00358; DSRW; 1.
DR PROSITE; PS0137; DS_RBD; 1.
KW Nonstructural protein; RNA-binding.
FT DOMAIN 384 400 DBEM.
SQ SEQUENCE 402 AA; 45081 MW; BFF553E9D955D49 CRC64;

Query Match          97.1%; Score 33; DB 1; Length 402;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAUC 5
Db 280 CHAIC 284
```

```
RESULT 39
VN34_ROTFC STANDARD; PRT; 402 AA.
AC P27586;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Nonstructural RNA-binding protein 34 (NS34) (NCVP4).
GN Name=S6;
OS Porcine rotavirus (group C / strain Cowden).
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=10916;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91361567; PubMed=1653496;
RA Qian Y.A., Jiang B.M., Saif L.J., Kang S.Y., Ojeh C.K., Green K.Y.;
RT "Molecular analysis of the gene 6 from a porcine group C rotavirus
RT that encodes the NS34 equivalent of group A rotaviruses.";
RL Virology 184:752-757(1991).
CC -!- SIMILARITY: Contains 1 DRBM (double-stranded RNA-binding) domain.
CC -----
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CC -----
DR EMBL; M69115; AAA47087.1; -.
DR F01R; A41040; MXXRPC.
DR InterPro; IPR001159; DS_RBD.
DR InterPro; IPR002873; Rota_NSP3.
DR Pfam; PF00035; dsrm; 1.
DR Pfam; PF01665; Rota_NSP3; 1.
DR PROSITE; PS50137; DS_RBD; 1.
KW Nonstructural protein; RNA-binding.
FT DOMAIN 384 400
SQ SEQUENCE 402 AA; 45125 MW; 8B11F7AC7FB5135C CRC64;

Query Match 97.1%; Score 33; DB 1; Length 402;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 280 CHAIC 284

RESULT 40
Q9PY95 PRELIMINARY; PRT; 402 AA.
AC Q9PY95;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nonstructural protein 3.
GN Name=NSP3;
OS Human rotavirus (group C / strain Bristol).
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus; Human rotavirus C.
OX NCBI_TaxID=31567;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol;
RX MEDLINE=20036633; PubMed=10567650;
RA James V.I.A., Lambden P.R., Deng Y., Caul E.O., Clarke I.N.;
RT "Molecular characterisation of human group C rotavirus genes 6, 7 and
RT 9.";
RL J. Gen. Virol. 80:3181-3187(1999).
DR EMBL; AJ132203; CAB52751.1; -.
DR HSSP; P03536; 1KNZ.
DR GO; GO:0005622; C:intracellular; IEA.
```

```
DR GO; GO:0019012; C:virion; IEA.
DR GO; GO:0003725; F:double-stranded RNA binding; IEA.
DR InterPro; IPR001159; DS_RBD.
DR InterPro; IPR002873; Rota_NSP3.
DR Pfam; PF00035; dsrm; 1.
DR Pfam; PF01665; Rota_NSP3; 1.
DR SMART; SM00358; DSRM; 1.
DR PROSITE; PS50137; DS_RBD; 1.
KW Nonstructural protein.
SQ SEQUENCE 402 AA; 45327 MW; D2E3D7F14B6E2E23 CRC64;

Query Match 97.1%; Score 33; DB 2; Length 402;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 280 CHAIC 284

RESULT 41
Q9M1Q8 PRELIMINARY; PRT; 428 AA.
AC Q9M1Q8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein T17J13.120.
GN Name=T17J13.120;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W.,
RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL138651; CAB71876.1; -.
DR PIR; T48008; T48008.
DR InterPro; IPR003480; Transferase.
DR Pfam; PF02458; Transferase; 1.
KW Hypothetical protein.
SQ SEQUENCE 428 AA; 47553 MW; 66C5155A161B26CA CRC64;

Query Match 97.1%; Score 33; DB 2; Length 428;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 153 CHAIC 157

RESULT 42
Q71159 PRELIMINARY; PRT; 665 AA.
AC Q71159;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural protein (Fragment).
GN Name=NS1;
OS Kilham rat virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX NCBI_TaxID=12441;
RN [1]
RP SEQUENCE FROM N.A.
```



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RC STRAIN=U-Mass;
RX MEDLINE=98184569; PubMed=9525656;
RA Ball-Goodrich L.J., Leland S.E., Johnson E.A., Patuzzo F.X.,
RA Jacoby R.O.;
RT "Rat parvovirus type 1: the prototype for a new rodent parvovirus
RT serogroup.";
RL J. Virol. 72:3289-3299(1998).
DR EMBL; AF036711; AAC40695.1; -.
DR GO; GO:0019012; C:virion; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR001257; Parvo_NSI.
DR Pfam; PF01057; Parvo_NSI; I.
KW Nonstructural protein.
FT NON TER 1
SQ SEQUENCE 665 AA; 75375 MW; 778E29043417E409 CRC64;

Query Match 97.1%; Score 33; DB 2; Length 665;
Best Local Similarity 80.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 371 CHAIC 375

RESULT 43
VNCS_PAVL3 STANDARD; PRT; 668 AA.
AC P36311;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Noncapsid protein NS-1 (Nonstructural protein NS1).
GN Name=NS1;
OS Parvovirus LuIII.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX NCBI_TaxID=35339;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=92297126; PubMed=8517025;
RA Diffoot N., Chen K.C., Bates R.C., Lederma M.;
RT "The complete nucleotide sequence of parvovirus LuIII and localization
RT of a unique sequence possibly responsible for its encapsidation
RT pattern.";
RL Virology 192:339-345(1993).
CC -1- FUNCTION: Seems necessary for viral DNA replication.
CC -1- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
CC -----
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CC -----
CC EMBL; M81888; -; NOT_ANNOTATED_CDS.
CC F04; A44276; A44276.
CC InterPro; IPR001257; Parvo_NSI.
CC Pfam; PF01057; Parvo_NSI; I.
CC ATP-binding; DNA replication; Noncapsid protein;
KW Nonstructural protein.
FT NP_BIND 399 406 ATP (Potential).
SQ SEQUENCE 668 AA; 75846 MW; CAE69049F8F6B53 CRC64;

Query Match 97.1%; Score 33; DB 1; Length 668;
Best Local Similarity 80.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 378 CHAIC 382

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RESULT 44
VNCS_MUMIV STANDARD; PRT; 672 AA.
ID VNCS_MUMIV STANDARD; PRT; 672 AA.
AC P07300; P10837;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVPI).
GN Name=NS1;
OS Murine minute virus (strain MVMi) (Murine parvovirus).
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX NCBI_TaxID=10795;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=86115415; PubMed=3502703;
RA Astell C.R., Gardiner E.M., Tattersall P.;
RT "DNA sequence of the lymphotropic variant of minute virus of mice,
RT MVM(1), and comparison with the DNA sequence of the fibrotropic
RT prototype strain.";
RL J. Virol. 57:656-669(1986).
RN [2];
RP SEQUENCE FROM N.A.
RX MEDLINE=85242059; PubMed=3855242;
RA Sahli R., McMaster G.K., Hirt B.;
RT "DNA sequence comparison between two tissue-specific variants of the
RT autonomous parvovirus, minute virus of mice.";
RL Nucleic Acids Res. 13:3617-3633(1985).
CC -1- FUNCTION: Seems necessary for viral DNA replication.
CC -1- SUBUNIT: Forms homooligomers. Interacts with human SYNCRIP (By
CC similarity).
CC -1- DOMAIN: The N-terminus (residues 1-275) possess a negative effect
CC on transactivation (By similarity).
CC -1- DOMAIN: The C-terminus (residues 543-672) possess an activation
CC domain (By similarity).
CC -1- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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CC -----
CC EMBL; X02481; -; NOT_ANNOTATED_CDS.
CC EMBL; M12032; AAA69567.1; -.
CC InterPro; IPR001257; Parvo_NSI.
CC Pfam; PF01057; Parvo_NSI; I.
CC ATP-binding; DNA replication; Noncapsid protein;
KW Nonstructural protein.
FT DOMAIN 1 276 Interacts with SYNCRIP (By similarity).
FT NP_BIND 399 406 ATP (Potential).
FT CONFLICT 597 597 I -> L (in Ref. 2).
SQ SEQUENCE 672 AA; 76140 MW; 25F025FE328B4DF0 CRC64;

Query Match 97.1%; Score 33; DB 1; Length 672;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 378 CHAIC 382

RESULT 45
VNCS_MUMIV STANDARD; PRT; 672 AA.
ID VNCS_MUMIV STANDARD; PRT; 672 AA.
AC P03134;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVPI).

```

GN Name=NS1;  
 OS Murine minute virus (Murine parvovirus).  
 OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.  
 OX NCBI\_TaxID=10794;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83143341; PubMed=6298737;  
 RA Astell C.R., Thomson M., Merchlinsky M., Ward D.C.;  
 RT "The complete DNA sequence of minute virus of mice, an autonomous  
 RT parvovirus.";  
 RL Nucleic Acids Res. 11:999-1018(1983).  
 RN [2]  
 RP HOMOLOGIZATION, AND INTERACTION WITH SYNCRIP.  
 RX MEDLINE=99102562; PubMed=9847309;  
 RA Harris C.E., Boden R.A., Astell C.R.;  
 RT "A novel heterogeneous nuclear ribonucleoprotein-like protein  
 RT interacts with NS1 of the minute virus of mice.";  
 RL J. Virol. 73:72-80(1999).  
 CC -1- FUNCTION: Seems necessary for viral DNA replication.  
 CC -1- SUBUNIT: Forms homooligomers. Interacts with human SYNCRIP.  
 CC -1- DOMAIN: The N-terminus (residues 1-275) possess a negative effect  
 CC on transactivation.  
 CC -1- DOMAIN: The C-terminus (residues 543-672) possess an activation  
 CC domain.  
 CC -1- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.  
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 CC -----  
 DR EMBL; J02275; AAA67109.1; -;  
 DR EMBL; V01115; CAA24309.1; ALT\_INIT.  
 DR PIR; A03696; UYPPVIM.  
 DR TRANSFAC; T02375; -;  
 DR InterPro; IPR001257; Parvo NS1.  
 DR Pfam; PF01057; Parvo NS1; 1.  
 KW ATP-binding; DNA replication; Noncapsid protein;  
 FT NP BIND 1 276 ATP (Potential).  
 FT NP BIND 399 406  
 SQ SEQUENCE 672 AA; 76248 MW; 50298F27662E3C1D CRC64;  
 Query Match 97.1%; Score 33; DB 1; Length 672;  
 Best Local Similarity 80.0%; Pred. No. 5.5e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CHAVC 5  
 DB 378 CHAIC 382  
 RESULT 46  
 VNCS\_PAVHH STANDARD; PRT; 672 AA.  
 AC P03133;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1).  
 GN Name=NS1;  
 OS Hamster parvovirus H1.  
 OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.  
 OX NCBI\_TaxID=10799;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83112183; PubMed=6823009;  
 RA Rhode S.L. III, Paradiso P.R.;  
 RT "Parvovirus genome: nucleotide sequence of H-1 and mapping of its  
 RT genes by hybrid-arrested translation.";

RL J. Virol. 45:173-184(1983).  
 CC -1- FUNCTION: Seems necessary for viral DNA replication.  
 CC -1- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.  
 CC -----  
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 CC -----  
 DR EMBL; X01457; CAA25689.1; -;  
 DR PIR; A03695; UYPPV1.  
 DR InterPro; IPR001257; Parvo NS1.  
 DR Pfam; PF01057; Parvo NS1; 1.  
 KW ATP-binding; DNA replication; Noncapsid protein;  
 KW Nonstructural protein.  
 FT NP BIND 399 406 ATP (Potential).  
 SQ SEQUENCE 672 AA; 75993 MW; 12F331142F72AA6D CRC64;  
 Query Match 97.1%; Score 33; DB 1; Length 672;  
 Best Local Similarity 80.0%; Pred. No. 5.5e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CHAVC 5  
 DB 378 CHAIC 382  
 RESULT 47  
 P88899 PRELIMINARY; PRT; 672 AA.  
 ID P88899  
 AC P88899;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Non-capsid protein.  
 GN Name=NS1;  
 OS Kilham rat virus.  
 OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.  
 OX NCBI\_TaxID=12441;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Brown D.W., Like A.A.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U79033; AAB38326.1; -;  
 DR GO; GO:0019079; P:Viral genome replication; IEA.  
 DR InterPro; IPR001257; Parvo NS1.  
 DR Pfam; PF01057; Parvo NS1; 1.  
 SQ SEQUENCE 672 AA; 76056 MW; 0299B36871A0A10A CRC64;  
 Query Match 97.1%; Score 33; DB 2; Length 672;  
 Best Local Similarity 80.0%; Pred. No. 5.5e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CHAVC 5  
 DB 378 CHAIC 382  
 RESULT 48  
 Q8JV14 PRELIMINARY; PRT; 672 AA.  
 ID Q8JV14  
 AC Q8JV14;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Nonstructural protein 1.  
 GN Name=NS1;  
 OS Rat minute virus 1c.  
 OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.  
 OX NCBI\_TaxID=172387;

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RN  SEQUENCE FROM N.A.
RX  MEDLINE=22120170; PubMed=12124471;
RA  Wan C.-H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
RT  "Molecular characterization of three newly recognized rat
RL  parvoviruses.";
RN  J. Gen. Virol. 83:2075-2083 (2002).
[1]
RP  SEQUENCE FROM N.A.
RA  Wan C.-H., Pintel D.J., Soderlund-Venermo M., Riley L.K.;
RL  Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF332884; AAM93279.1; -.
DR  GO; GO:0019012; C:virion; IEA.
DR  GO; GO:0019079; P:viral genome replication; IEA.
DR  InterPro; IPR001257; Parvo.NS1.
DR  Pfam; PF01057; Parvo.NS1; I.
KW  Nonstructural protein.
SQ  SEQUENCE 672 AA; 75988 MW; 52DF6549349CF3FD CRC64;

Query Match          97.1%; Score 33; DB 2; Length 672;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1 CHAVC 5
Db  378 CHAIC 382

RESULT 49
Q8JV16
ID  Q8JV16          PRELIMINARY;      PRT;    672 AA.
AC  Q8JV16;
DT  01-OCT-2002 (TrEMBLrel. 22, Created)
DT  01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  Nonstructural protein 1.
GN  Name=NS1;
OS  Rat minute virus 1b.
OC  Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX  NCBI_TaxID=172386;
[1]
RP  SEQUENCE FROM N.A.
RA  Wan C.-H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
RT  "Molecular characterization of three newly recognized rat
RL  parvoviruses.";
RN  J. Gen. Virol. 83:2075-2083 (2002).
[2]
RP  SEQUENCE FROM N.A.
RA  Wan C.-H., Pintel D.J., Soderlund-Venermo M., Riley L.K.;
RL  Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF332883; AAM93277.1; -.
DR  GO; GO:0019012; C:virion; IEA.
DR  GO; GO:0019079; P:viral genome replication; IEA.
DR  InterPro; IPR001257; Parvo.NS1.
DR  Pfam; PF01057; Parvo.NS1; I.
KW  Nonstructural protein.
SQ  SEQUENCE 672 AA; 76201 MW; C2F1A71F6EF449A6 CRC64;

Query Match          97.1%; Score 33; DB 2; Length 672;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1 CHAVC 5
Db  378 CHAIC 382

RESULT 50
Q8JV18
ID  Q8JV18          PRELIMINARY;      PRT;    672 AA.
AC  Q8JV18;
DT  01-OCT-2002 (TrEMBLrel. 22, Created)

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DT  01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  Nonstructural protein 1.
GN  Name=NS1;
OS  Rat minute virus 1a.
OC  Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX  NCBI_TaxID=172385;
[1]
RP  SEQUENCE FROM N.A.
RA  Wan C.-H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
RL  Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF332882; AAM93275.1; -.
DR  GO; GO:0019012; C:virion; IEA.
DR  GO; GO:0019079; P:viral genome replication; IEA.
DR  InterPro; IPR001257; Parvo.NS1.
DR  Pfam; PF01057; Parvo.NS1; I.
KW  Nonstructural protein.
SQ  SEQUENCE 672 AA; 76059 MW; 63D8B9BFP99E07B3 CRC64;

Query Match          97.1%; Score 33; DB 2; Length 672;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1 CHAVC 5
Db  378 CHAIC 382

RESULT 51
Q8JV28
ID  Q8JV28          PRELIMINARY;      PRT;    672 AA.
AC  Q8JV28;
DT  01-OCT-2002 (TrEMBLrel. 22, Created)
DT  01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  Nonstructural protein 1.
GN  Name=ns1;
OS  Kilham rat virus.
OC  Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX  NCBI_TaxID=12441;
[1]
RP  SEQUENCE FROM N.A.
RA  Wan C.-H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
RL  Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF321230; AAM93272.1; -.
DR  GO; GO:0019012; C:virion; IEA.
DR  GO; GO:0019079; P:viral genome replication; IEA.
DR  InterPro; IPR001257; Parvo.NS1.
DR  Pfam; PF01057; Parvo.NS1; I.
KW  Nonstructural protein.
SQ  SEQUENCE 672 AA; 75987 MW; 22B4611C20CDB6E9 CRC64;

Query Match          97.1%; Score 33; DB 2; Length 672;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1 CHAVC 5
Db  378 CHAIC 382

```

## RESULT 52

Q83429 Q83429 PRELIMINARY; PRT; 672 AA.  
AC Q83429;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Nonstructural protein 1.  
GN Name=NS1;  
OS Mouse parvovirus 1.  
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.  
OX NCBI\_TaxID=35340;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94365951; PubMed=8083985;  
RA Ball-Goodrich L.J., Johnson E.;  
RT "Molecular characterization of a newly recognized mouse parvovirus.";  
RL J. Virol. 68:6476-6486(1994).  
DR EMBL; U12469; AAA61405.1; -.  
DR GO; GO:0019012; C:virion; IEA.  
DR GO; GO:0019079; P:Viral genome replication; IEA.  
DR InterPro; IPR001257; Parvo NS1.  
DR Pfam; PF01057; Parvo NS1; I.  
KW Nonstructural protein.  
SQ SEQUENCE 672 AA; 76112 MW; 31C6365276727363 CRC64;

Query Match 97.1%; Score 33; DB 2; Length 672;  
Best Local Similarity 80.0%; Pred. No. 5.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 378 CHAIC 382

## RESULT 53

Q84363 Q84363 PRELIMINARY; PRT; 721 AA.  
AC Q84363;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Nonstructural protein.  
GN Name=NS1;  
OS Murine minute virus (Murine parvovirus).  
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.  
OX NCBI\_TaxID=10794;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86115415; PubMed=3502703;  
RA Astell C.R., Gardiner E.M., Tattersall P.;  
RT "DNA sequence of the lymphotropic variant of minute virus of mice, MVM(1), and comparison with the DNA sequence of the fibrotropic prototype strain".  
RT J. Virol. 57:656-669(1986).  
RL EMBL; M12032; AAA69566.1; -.  
DR PIR; A23008; UYFVIN.  
DR GO; GO:0019012; C:virion; IEA.  
DR GO; GO:0019079; P:Viral genome replication; IEA.  
DR InterPro; IPR001257; Parvo NS1.  
DR Pfam; PF01057; Parvo NS1; I.  
KW Nonstructural protein.  
SQ SEQUENCE 721 AA; 81862 MW; 9FD29C327C7F4BBF CRC64;

Query Match 97.1%; Score 33; DB 2; Length 721;  
Best Local Similarity 80.0%; Pred. No. 5.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 427 CHAIC 431

## RESULT 54

Q84365 Q84365 PRELIMINARY; PRT; 721 AA.  
AC Q84365;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Nonstructural protein.  
GN Name=NS1;  
OS Murine minute virus (Murine parvovirus).  
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.  
OX NCBI\_TaxID=10794;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=MVM;  
RX MEDLINE=83143341; PubMed=6298737;  
RA Astell C.R., Thomson M., Merchlinsky M., Ward D.C.;  
RT "The complete DNA sequence of minute virus of mice, an autonomous parvovirus".  
RT Nucleic Acids Res. 11:999-1018(1983).  
RL [2]  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=MVM;  
RX MEDLINE=86115415; PubMed=3502703;  
RA Astell C.R., Gardiner E.M., Tattersall P.;  
RT "DNA sequence of the lymphotropic variant of minute virus of mice, MVM(1), and comparison with the DNA sequence of the fibrotropic prototype strain".  
RT J. Virol. 57:656-669(1986).  
RL [3]  
RN [3]  
RP SEQUENCE FROM N.A.

RC STRAIN=MVM;  
RX MEDLINE=87061199; PubMed=3783817;  
RA Morgan W.R., Ward D.C.;  
RT "Three splicing patterns are used to excise the small intron common to all minute virus of mice RNAs".  
RL J. Virol. 60:1170-1174(1986).  
DR EMBL; J02275; AAA67108.1; -.  
DR GO; GO:0019012; C:virion; IEA.  
DR GO; GO:0019079; P:Viral genome replication; IEA.  
DR InterPro; IPR001257; Parvo NS1.  
DR Pfam; PF01057; Parvo NS1; I.  
KW Nonstructural protein.  
SQ SEQUENCE 721 AA; 81896 MW; 18391758E42F0DCF CRC64;

Query Match 97.1%; Score 33; DB 2; Length 721;  
Best Local Similarity 80.0%; Pred. No. 5.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 427 CHAIC 431

## RESULT 55

Q6ES22 Q6ES22 PRELIMINARY; PRT; 815 AA.  
AC Q6ES22;  
DT 25-OCT-2004 (TReMBLrel. 28, Created)  
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
DE Putative far-red impaired response protein.  
GN Name=P0472F10.13-1;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sasaki T., Matsumoto T., Yamamoto K.;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP004877; BAD28228.1; -

DR GO; GO:0003677; F:DNA binding; IEA.

DR InterPro; IPR004330; FAR1.

DR InterPro; IPR003657; WRKY.

DR InterPro; IPR006564; Znf\_PMZ.

DR InterPro; IPR007527; Znf\_SWIM.

DR Pfam; PF03101; FAR1; 1.

DR Pfam; PF04434; SWIM; 1.

DR SMART; SM00575; Znf\_PMZ; 1.

DR PROSITE; PS00811; WRKY; 1.

SQ SEQUENCE 815 AA; 92895 MW; 003FD2ED7784E1C4 CRC64;

Query Match 97.1%; Score 33; DB 2; Length 815;

Best Local Similarity 80.0%; Pred. No. 6.5e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 352 CHAIC 356

RESULT 56

Q7XDU9 PRELIMINARY; PRT; 929 AA.

AC Q1-XDU9;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Putative mutator protein.

GN ORFNames=OSJNBa0068N06.23;

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Eriarthroideae; Oryzeae; Oryza.

OX NCBI\_TaxID=39947;

RN [1]

RP SEQUENCE FROM N.A.

RA The Rice Chromosome 10 Sequencing Consortium;

RT "In-depth view of structure, activity, and evolution of rice

chromosome 10."

RL Science 300:1566-1569(2003).

RN [2]

RP SEQUENCE FROM N.A.

RA Buell C.R., Wing R.A., McCambie W.R., Messing J., Yuan Q.;

RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE017100; AAP54042.1; -

DR Gramene; Q7XDU9; -

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR InterPro; IPR001878; Znf\_CCHC.

DR Pfam; PF00098; zf-CCHC; 1.

DR SMART; SM00343; Znf\_C2HC; 1.

SQ SEQUENCE 929 AA; 104564 MW; FB8FAD5D49F09300 CRC64;

Query Match 97.1%; Score 33; DB 2; Length 929;

Best Local Similarity 80.0%; Pred. No. 7.4e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 719 CHAIC 723

RESULT 57

Q6L4D3 PRELIMINARY; PRT; 1092 AA.

AC Q6L4D3;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein OSJNBa0088M05.7;

GN Name=OSJNBa0088M05.7;

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Eriarthroideae; Oryzeae; Oryza.

OX NCBI\_TaxID=39947;

RN [1]

RP SEQUENCE FROM N.A.

RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,

RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,

RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,

RA Hsiung J.-N., Heu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,

RA Li Y.-P., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,

RA Wu H.-P., Shaw J.-P.,

RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC136222; AAT38055.1; -

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR InterPro; IPR001878; Znf\_CCHC.

DR InterPro; IPR006564; Znf\_PMZ.

DR InterPro; IPR007527; Znf\_SWIM.

DR Pfam; PF04434; SWIM; 1.

DR Pfam; PF00098; zf-CCHC; 1.

DR SMART; SM00575; Znf\_PMZ; 1.

KW Hypothetical protein.

SQ SEQUENCE 1092 AA; 122243 MW; 8A9B50FD758C0EA5 CRC64;

Query Match 97.1%; Score 33; DB 2; Length 1092;

Best Local Similarity 80.0%; Pred. No. 8.5e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 805 CHAIC 809

RESULT 58

SCX1\_MESTA

ID SCX1\_MESTA STANDARD; PRT; 64 AA.

AC P60277;

DT 29-MAR-2004 (Rel. 43, Created)

DT 29-MAR-2004 (Rel. 43, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Neurotoxin.

OS Mesobuthus tamulus (Eastern Indian scorpion) (Buthus tamulus).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;

OC Buthida; Buthoidea; Buthidae; Mesobuthus.

OX NCBI\_TaxID=34647;

RN [1]

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).

RA Sharma M., Yadav S., Karthikeyan S., Kumar S., Paramasivam M.,

RA Srinivasan A., Singh T.P.;

RT "Three-dimensional structure of a neurotoxin from red scorpion (Buthus

tamulus) at 2.2-A resolution."

RL Submitted (AUG-2000) to the PDB data bank.

CC -1- FUNCTION: Inhibits sodium channels (By similarity).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -1- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

DR PDB; 1DO7; X-ray; -

DR InterPro; IPR002061; Scorpion\_toxinL.

DR PRINTS; PR00285; SCORPNTXIN.

DR ProDom; PD000908; Scorpion\_toxinL; 1.

KW 3D-structure; Ionic channel inhibitor; Neurotoxin;

KW Sodium channel inhibitor; Toxin.

FT DISULFID 12 63

FT DISULFID 16 36

FT DISULFID 22 46

FT DISULFID 26 48

SQ SEQUENCE 64 AA; 7041 MW; 06A852E2F5B0B934 CRC64;

Query Match 91.2%; Score 31; DB 1; Length 64;

Best Local Similarity 80.0%; Pred. No. 1.4e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

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Db          |||:|
           22 CHALC 26

RESULT 59
Q8D488      PRELIMINARY;          PRT; 108 AA.
AC Q8D488;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=VW21423;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
  Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AS016813; AAO08302.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 108 AA; 11846 MW; FB92F8EA3E170EAA CRC64;

Query Match          91.2%; Score 31; DB 2; Length 108;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
    ||:|
Db 57 CHSVC 61

RESULT 60
Q7MFR2      PRELIMINARY;          PRT; 116 AA.
AC Q7MFR2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein VWA0258.
GN OrderedLocusNames=VWA0258;
OS Vibrio vulnificus (strain YJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
  Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
  Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
  pathogen.";
RL Genome Res. 13:2577-2587(2003).
DR EMBL; AP005345; BAC96284.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 116 AA; 12693 MW; 19B1D5E12C9C108B CRC64;

Query Match          91.2%; Score 31; DB 2; Length 116;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
    ||:|
Db 65 CHSVC 69

RESULT 61
Q8C3T4      PRELIMINARY;          PRT; 118 AA.
AC Q8C3T4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched
  library, clone:D430021L16 product:hypothetical protein, full insert
  sequence.
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX The FANTOM Consortium;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
  60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
  Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
  prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
  Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
  Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
  Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
  Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
  Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
  Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
  sequencing pipeline with 384 multipipillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
  Fukuda S., Furuno M., Hanegaki T., Hara A., Hashizume W.,
  Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
  Hori F., Imotani K., Itoh Y., Itoh M., Kagawa I., Kasukawa T.,
  Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
  Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
  Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
  Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
  Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
  Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
  Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RL

```

DR EMBL; AK084985; BAC39329.1; --  
 KW Hypothetical protein.  
 SQ SEQUENCE 118 AA; 12409 MW; 9DE6A7E88C8575BC CRC64;  
 Query Match 91.2%; Score 31; DB 2; Length 118;  
 Best Local Similarity 80.0%; Pred. No. 2.5e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CHAVC 5  
 Db 114 CHALC 118  
 RESULT 62  
 Q8QY23  
 ID Q8QY23 PRELIMINARY; PRT; 124 AA.  
 AC Q8QY23;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Thymidylate synthase-like protein.  
 OS Rana tigrina ranavirus.  
 OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Ranavirus.  
 OX NCBI\_TaxID=160691;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21874850; PubMed=11878922; DOI=10.1006/viro.2001.1245;  
 RA He J.G., Lu L., Deng M., He H.H., Weng S.P., Wang X.H., Zhou S.Y.,  
 RA Long Q.X., Wang X.Z., Chan S.M.;  
 RA "Sequence analysis of the complete genome of an iridovirus isolated  
 RT from the tiger frog."  
 RL Virology 292:185-197(2002).  
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =  
 CC -1- dihydrofolate + dTMP.  
 CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.  
 CC -1- SIMILARITY: Belongs to the thymidylate synthase family.  
 CC EMBL; AF389451; AAL77812.1; --  
 DR HSSP; P45352; 1RFS.  
 DR GO; GO:0008168; P:methyltransferase activity; IEA.  
 DR GO; GO:0004799; P:thymidylate synthase activity; IEA.  
 DR GO; GO:0016740; P:transferase activity; IEA.  
 DR GO; GO:0006231; P:dTMP biosynthesis; IEA.  
 DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.  
 DR InterPro; IPR000398; Thymidylat synth.  
 DR Pfam; PF00303; Thymidylat synt; 1.  
 DR PRINTS; PR00108; THYMSNTHASE.  
 DR ProDom; PD001180; Thymidylat synth; 1.  
 DR KW Methyltransferase; Nucleotide biosynthesis; Transferase.  
 SQ SEQUENCE 124 AA; 14002 MW; 7123A290B15E6D21 CRC64;  
 Query Match 91.2%; Score 31; DB 2; Length 124;  
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CHAVC 5  
 Db 6 CHAMC 10  
 RESULT 63  
 Q8TWX8  
 ID Q8TWX8 PRELIMINARY; PRT; 139 AA.  
 AC Q8TWX8;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Ferredoxin.  
 GN OrderedLocusNames=MK0903;  
 OS Methanopyrus kandleri.  
 OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;  
 OC Methanopyrus.  
 OX NCBI\_TaxID=2320;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=AV19 / DSM 6324 / JCM 9639;  
 RX MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;  
 RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,  
 RA Shcherbina O.V., Shakhova V.V., Belova G.I., Aravind L.,  
 RA Nacale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,  
 RA Malykh A.G., Koonin E.V., Kozlyavkin S.A.;  
 RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19  
 RT and monophyly of archaeal methanogens."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).  
 DR EMBL; AE010380; AAM02116.1; --  
 DR HSSP; P00193; 1DUR.  
 DR GO; GO:0005489; F:electron transporter activity; IEA.  
 DR GO; GO:0005506; F:iron ion binding; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR Pfam; PF00037; Fer4; 2.  
 DR PRINTS; PR00353; 4FE4SPRDOXIN  
 DR PROSITE; PS00198; 4FE4S FERREDOXIN; 2.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN 1.  
 KW 4FC-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding.  
 SQ SEQUENCE 139 AA; 15190 MW; CE929F07722287FE CRC64;  
 Query Match 91.2%; Score 31; DB 2; Length 139;  
 Best Local Similarity 80.0%; Pred. No. 2.9e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CHAVC 5  
 Db 91 CHSVC 95  
 RESULT 64  
 Q91019  
 ID Q91019 PRELIMINARY; PRT; 168 AA.  
 AC Q91019;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE TRLU10.  
 OS Human cytomegalovirus.  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Betaherpesvirinae; Cytomegalovirus.  
 OX NCBI\_TaxID=10359;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=11pan, Davis, and 33spa;  
 RX MEDLINE=21635521; PubMed=11734418;  
 RA Spaderna S., Blessing H., Bogner E., Britt W., Mach M.;  
 RT "Identification of glycoprotein gpTRLU10 as a structural component of  
 RT human cytomegalovirus."  
 RL J. Virol. 76:1450-1460(2002).  
 DR EMBL; AF432091; AAL27473.1; --  
 DR EMBL; AF432084; AAL27466.1; --  
 DR EMBL; AF432087; AAL27469.1; --  
 DR Pfam; PF06084; Cytomega TRLU10; 1.  
 DR SQ SEQUENCE 168 AA; 18762 MW; B18FA2748C12F431 CRC64;  
 Query Match 91.2%; Score 31; DB 2; Length 168;  
 Best Local Similarity 80.0%; Pred. No. 3.5e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CHAVC 5  
 Db 57 CHAMC 61  
 RESULT 65  
 Q6SX91  
 ID Q6SX91 PRELIMINARY; PRT; 168 AA.  
 AC Q6SX91;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE RL10.  
 OS Human cytomegalovirus.  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Betaherpesvirinae; Cytomegalovirus.  
 OX NCBI\_TaxID=10359;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=6397;  
 RX PubMed=15105547; DOI=10.1099/vir.0.79888-0;  
 RA Dolan A., Cunningham C., Hector R.D., Hassan-Walker A.F., Lee L.,  
 RA Addison C., Dargan D.J., McGeoch D.J., Gatherer D., Emery V.C.,  
 RA Griffiths P.D., Sinzger C., McSharry B.P., Wilkinson G.W.,  
 RA Davison A.J.;  
 RT "Genetic content of wild-type human cytomegalovirus.";  
 RL J. Gen. Virol. 85:1301-1312(2004).  
 DR EMBL; AY446861; AAR31252.1; -.  
 DR InterPro; IPR009284; Cytomega\_TRL10.  
 DR Pfam; PF06084; Cytomega\_TRL10; 1.  
 SQ SEQUENCE 168 AA; 18776 MW; B18FA2748C144281 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 168;  
 Best Local Similarity 80.0%; Pred. No. 3.5e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
 |||:|  
 Db 57 CHAMC 61

## RESULT 66

ID Q6SXA8 PRELIMINARY; PRT; 168 AA.  
 AC Q6SXA8;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE RL10.  
 OS Human cytomegalovirus.  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Betaherpesvirinae; Cytomegalovirus.  
 OX NCBI\_TaxID=10359;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Toledo;  
 RX PubMed=15105547; DOI=10.1099/vir.0.79888-0;  
 RA Dolan A., Cunningham C., Hector R.D., Hassan-Walker A.F., Lee L.,  
 RA Addison C., Dargan D.J., McGeoch D.J., Gatherer D., Emery V.C.,  
 RA Griffiths P.D., Sinzger C., McSharry B.P., Wilkinson G.W.,  
 RA Davison A.J.;  
 RT "Genetic content of wild-type human cytomegalovirus.";  
 RL J. Gen. Virol. 85:1301-1312(2004).  
 DR EMBL; AY446860; AAR31235.1; -.  
 DR InterPro; IPR009284; Cytomega\_TRL10.  
 DR Pfam; PF06084; Cytomega\_TRL10; 1.  
 SQ SEQUENCE 168 AA; 18763 MW; CODA9297670DAD86 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 168;  
 Best Local Similarity 80.0%; Pred. No. 3.5e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
 |||:|  
 Db 57 CHAMC 61

## RESULT 67

ID Q914P6 PRELIMINARY; PRT; 170 AA.  
 AC Q914P6;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE TRL10.

OS Human cytomegalovirus.  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Betaherpesvirinae; Cytomegalovirus.  
 OX NCBI\_TaxID=10359;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=22alt;  
 RX MEDLINE=21635521; PubMed=11773418;  
 RA Spaderna S., Blessing H., Bogner E., Britt W., Mach M.;  
 RT "Identification of glycoprotein gpTRL10 as a structural component of  
 human cytomegalovirus.";  
 RL J. Virol. 76:1450-1460(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Merlin;  
 RX PubMed=15105547; DOI=10.1099/vir.0.79888-0;  
 RA Dolan A., Cunningham C., Hector R.D., Hassan-Walker A.F., Lee L.,  
 RA Addison C., Dargan D.J., McGeoch D.J., Gatherer D., Emery V.C.,  
 RA Griffiths P.D., Sinzger C., McSharry B.P., Wilkinson G.W.,  
 RA Davison A.J.;  
 RT "Genetic content of wild-type human cytomegalovirus.";  
 RL J. Gen. Virol. 85:1301-1312(2004).  
 DR EMBL; AY432089; AAL27471.1; -.  
 DR EMBL; AY446894; AAR31564.1; -.  
 DR Pfam; PF06084; Cytomega\_TRL10; 1.  
 SQ SEQUENCE 170 AA; 18974 MW; 7C850AB8EF36E61C CRC64;

Query Match 91.2%; Score 31; DB 2; Length 170;  
 Best Local Similarity 80.0%; Pred. No. 3.5e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
 |||:|  
 Db 59 CHAMC 63

## RESULT 68

ID Q914P8 PRELIMINARY; PRT; 170 AA.  
 AC Q914P8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE TRL10.  
 OS Human cytomegalovirus.  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Betaherpesvirinae; Cytomegalovirus.  
 OX NCBI\_TaxID=10359;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=7ro;  
 RX MEDLINE=21635521; PubMed=11773418;  
 RA Spaderna S., Blessing H., Bogner E., Britt W., Mach M.;  
 RT "Identification of glycoprotein gpTRL10 as a structural component of  
 human cytomegalovirus.";  
 RL J. Virol. 76:1450-1460(2002).  
 DR EMBL; AF432085; AAL27467.1; -.  
 DR Pfam; PF06084; Cytomega\_TRL10; 1.  
 SQ SEQUENCE 170 AA; 19031 MW; 7B7827917BFCB80C CRC64;

Query Match 91.2%; Score 31; DB 2; Length 170;  
 Best Local Similarity 80.0%; Pred. No. 3.5e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
 |||:|  
 Db 59 CHAMC 63

## RESULT 69

ID Q914P9 PRELIMINARY; PRT; 170 AA.  
 AC Q914P9;



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DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE TRL10
OS Human cytomegalovirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=7330et;
RX MEDLINE=21635521; PubMed=11773418;
RA Spaderna S., Blessing H., Bogner E., Britt W., Mach M.;
RT "Identification of glycoprotein gpTRL10 as a structural component of
human cytomegalovirus.";
RL J. Virol. 76:1450-1460(2002).
DR EMBL; AF432083; AAL27465.1; -.
DR Pfam; PF06084; Cytomega_TRL10; 1.
SQ SEQUENCE 170 AA; 19032 MW; 7B76C7917BFCB80C CRC64;

Query Match 91.2%; Score 31; DB 2; Length 170;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 59 CHAMC 63

RESULT 70
ID IR10 HCMVA STANDARD; PRT; 171 AA.
AC P16808;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Hypothetical protein IRL10 precursor (TRL10).
OS Human cytomegalovirus (strain AD169).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10360;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90269039; PubMed=2161319;
RA Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
RA Horsnell T., Hutchinson C.A. III, Kouzarides T., Martignetti J.A.,
RA Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
RT "Analysis of the protein-coding content of the sequence of human
cytomegalovirus strain AD169.";
RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@iesb-sib.ch).
CC -----
DR EMBL; X17403; CRA35300.1; -.
DR PIR; S09903; S09903.
DR InterPro; IPR009284; Cytomega_TRL10.
DR Pfam; PF06084; Cytomega_TRL10; 1.
KW Glycoprotein, Hypothetical protein; Signal; Transmembrane.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 171 Hypothetical protein IRL10.
FT TRANSMEM 80 100 Potential.
FT CARBOHYD 48 48 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 56 56 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 171 AA; 19034 MW; 2C2E8AD869419B86 CRC64;

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Query Match 91.2%; Score 31; DB 1; Length 171;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 60 CHAMC 64

RESULT 71
ID Q914P7 PRELIMINARY; PRT; 171 AA.
AC Q914P7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE TRL10.
OS Human cytomegalovirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5929C;
RX MEDLINE=21635521; PubMed=11773418;
RA Spaderna S., Blessing H., Bogner E., Britt W., Mach M.;
RT "Identification of glycoprotein gpTRL10 as a structural component of
human cytomegalovirus.";
RL J. Virol. 76:1450-1460(2002).
DR EMBL; AF432088; AAL27470.1; -.
DR Pfam; PF06084; Cytomega_TRL10; 1.
SQ SEQUENCE 171 AA; 19035 MW; 2C206AD869419B86 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 171;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 60 CHAMC 64

RESULT 72
ID Q69029 PRELIMINARY; PRT; 171 AA.
AC Q69029; OTM5U1;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE HCMVTRL10 = IRL10 protein.
GN Name=HCMVTRL10 = IRL10;
OS Human cytomegalovirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AD169;
RX MEDLINE=90269039; PubMed=2161319;
RA Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
RA Horsnell T., Hutchinson III C.A., Kouzarides T., Martignetti J.A.,
RA Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
RT "Analysis of the protein coding content of human cytomegalovirus
strain AD169.";
RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AD169;
RX MEDLINE=92199238; PubMed=1666311;
RA Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Chee M.S.,
RA Hutchinson III C.A., Kouzarides T., Martignetti J.A., Preddie E.,
RA Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
RT "The DNA sequence of the human cytomegalovirus genome.";

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RL DNA Seq. 2:1-12(1991).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AD169;  
RA Chee M.;  
RL Submitted (DEC-1989) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AD169;  
RX MEDLINE=22421467; PubMed=12533697; DOI=10.1099/vir.0.18606-0;  
RA Davison A.J., Dolan A., Akter P., Addison C., Dargan D.J.,  
RA Alcendor D.J., McGeoch D.J., Hayward G.S.;  
RT "The human cytomegalovirus genome revisited: comparison with the  
RT chimpanzee cytomegalovirus genome.";  
RL J. Gen. Virol. 84:17-28(2003).  
DR EMBL; X17403; CAA35458.1; -.  
DR EMBL; BK000394; DAA00091.1; -.  
DR PIR; S09759;  
DR InterPro; IPR009284; Cytomega\_TRL10.  
DR Pfam; PF06084; Cytomega\_TRL10; 1.  
SQ SEQUENCE 171 AA; 13035 MW; AE2E8AD0CB47D988 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 171;  
Best Local Similarity 80.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||:|  
Db 60 CHAMC 64

## RESULT 73

Q6SX75  
ID Q6SX75 PRELIMINARY; PRT; 171 AA.  
AC Q6SX75;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (T-EMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (T-EMBlrel. 27, Last annotation update)  
DE RL10.  
OS Human cytomegalovirus.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Betaherpesvirinae; Cytomegalovirus.  
OX NCBI\_TaxID=10359;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=3301;  
RX PubMed=15105547; DOI=10.1099/vir.0.79888-0;  
RA Dolan A., Cunningham C., Hector R.D., Hassan-Walker A.F., Lee L.,  
RA Addison C., Dargan D.J., McGeoch D.J., Gatherer D., Emery V.C.,  
RA Griffiths P.D., Sinzger C., McSharry B.P., Wilkinson G.W.,  
RA Davison A.J.;  
RT "Genetic content of wild-type human cytomegalovirus.";  
RL J. Gen. Virol. 85:1301-1312(2004).  
DR EMBL; AY446862; AAR31268.1; -.  
DR InterPro; IPR009284; Cytomega\_TRL10.  
DR Pfam; PF06084; Cytomega\_TRL10; 1.  
SQ SEQUENCE 171 AA; 13016 MW; 23F9220850767596 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 171;  
Best Local Similarity 80.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||:|  
Db 60 CHAMC 64

## RESULT 74

Q6SXC6  
ID Q6SXC6 PRELIMINARY; PRT; 171 AA.  
AC Q6SXC6;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (T-EMBlrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE RL10.  
OS Human cytomegalovirus.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Betaherpesvirinae; Cytomegalovirus.  
OX NCBI\_TaxID=10359;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=3;  
RX PubMed=15105547; DOI=10.1099/vir.0.79888-0;  
RA Dolan A., Cunningham C., Hector R.D., Hassan-Walker A.F., Lee L.,  
RA Addison C., Dargan D.J., McGeoch D.J., Gatherer D., Emery V.C.,  
RA Griffiths P.D., Sinzger C., McSharry B.P., Wilkinson G.W.,  
RA Davison A.J.;  
RT "Genetic content of wild-type human cytomegalovirus.";  
RL J. Gen. Virol. 85:1301-1312(2004).  
DR EMBL; AY446859; AAR31217.1; -.  
DR InterPro; IPR009284; Cytomega\_TRL10.  
DR Pfam; PF06084; Cytomega\_TRL10; 1.  
SQ SEQUENCE 171 AA; 19006 MW; CDA4427AE376BE25 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 171;  
Best Local Similarity 80.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||:|  
Db 60 CHAMC 64

## RESULT 75

Q7M6G1  
ID Q7M6G1 PRELIMINARY; PRT; 171 AA.  
AC Q7M6G1;  
DT 01-MAR-2004 (TREMBlrel. 26, Created)  
DT 01-MAR-2004 (T-EMBlrel. 26, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE RL10.  
OS Human cytomegalovirus.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Betaherpesvirinae; Cytomegalovirus.  
OX NCBI\_TaxID=10359;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AD169;  
RX MEDLINE=22421467; PubMed=12533697; DOI=10.1099/vir.0.18606-0;  
RA Davison A.J., Dolan A., Akter P., Addison C., Dargan D.J.,  
RA Alcendor D.J., McGeoch D.J., Hayward G.S.;  
RT "The human cytomegalovirus genome revisited: comparison with the  
RT chimpanzee cytomegalovirus genome.";  
RL J. Gen. Virol. 84:17-28(2003).  
CC -!- MISCELLANEOUS: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.  
DR EMBL; BK000394; DAA00228.1; -.  
DR InterPro; IPR009284; Cytomega\_TRL10.  
DR Pfam; PF06084; Cytomega\_TRL10; 1.  
SQ SEQUENCE 171 AA; 19034 MW; 2C2E8AD869419B86 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 171;  
Best Local Similarity 80.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||:|  
Db 60 CHAMC 64

## RESULT 76

Q8C2H6  
ID Q8C2H6 PRELIMINARY; PRT; 222 AA.  
AC Q8C2H6;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (T-EMBlrel. 23, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430021G10 product:thymidylate synthase, full insert sequence. (Fragment).  
GN Name=Tyms;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN  
RP  
SEQUENCE FROM N.A.  
RC STRAIN=NOND; TISSUE=Thymus;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning."  
RL Meth. Enzymol. 303:19-44(1999).  
[2]  
RN  
RP  
SEQUENCE FROM N.A.  
RC STRAIN=NOND; TISSUE=Thymus;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA RIKEN PANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
[3]  
RN  
RP  
SEQUENCE FROM N.A.  
RC STRAIN=NOND; TISSUE=Thymus;  
RX The PANTOM Consortium;  
RT the RIKEN Genome Exploration Research Group Phase I & II Team;  
RL "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."  
RL Nature 420:563-573(2002).  
[4]  
RN  
RP  
SEQUENCE FROM N.A.  
RC STRAIN=NOND; TISSUE=Thymus;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."  
RL Genome Res. 10:1617-1630(2000).  
[5]  
RN  
RP  
SEQUENCE FROM N.A.  
RC STRAIN=NOND; TISSUE=Thymus;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sakaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M., Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."  
RL Genome Res. 10:1757-1771(2000).  
[6]  
RN  
RP  
SEQUENCE FROM N.A.  
RC STRAIN=NOND; TISSUE=Thymus;  
RX Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Katukawa T., Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP = dihydrofolate + dTMP.  
CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.  
CC -!- SIMILARITY: Belongs to the thymidylate synthase family.

DR EMBL; AK086066; BAC40450.1; --  
DR HSPD; P04818; IHW3.  
DR MGSD; MGI:98878; Tyms.  
DR GO; GO:000168; P:thymidylate synthase activity; IEA.  
DR GO; GO:0004799; P:transferase activity; IEA.  
DR GO; GO:0016740; P:transferase activity; IEA.  
DR GO; GO:0006231; P:dTMP biosynthesis; IEA.  
DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.  
DR InterPro; IPR000398; Thymidylat synth.  
DR Pfam; PF00303; Thymidylat synth.  
DR PRINTS; PR00108; THYMSYNTHASE.  
DR PRODOM; PD001180; Thymidylat synth.  
DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.  
KW Methyltransferase; Nucleotide biosynthesis; Transferase.  
FT NON TER 1  
SQ SEQUENCE 222 AA; 25133 MW; 300157EB7AC78CA5 CRC64;  
  
Query Match 91.2%; Score 31; DB 2; Length 222;  
Best Local Similarity 80.0%; Pred. No. 4.5e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 0;  
  
Qy 1 CHAVC 5  
Db 104 CHALC 108  
|||  
|||  
  
RESULT 77  
Q8C2R3 PRELIMINARY; PRT; 222 AA.  
AC Q8C2R3  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430004M05 product:thymidylate synthase, full insert sequence. (Fragment).  
DE Name=Tyms;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN  
RP  
SEQUENCE FROM N.A.  
RC STRAIN=NOND; TISSUE=Thymus;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning."  
RL Meth. Enzymol. 303:19-44(1999).  
[2]  
RN  
RP  
SEQUENCE FROM N.A.  
RC STRAIN=NOND; TISSUE=Thymus;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA RIKEN PANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
[3]  
RN  
RP  
SEQUENCE FROM N.A.  
RC STRAIN=NOND; TISSUE=Thymus;  
RX The PANTOM Consortium;  
RT the RIKEN Genome Exploration Research Group Phase I & II Team;  
RL "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."  
RL Nature 420:563-573(2002).  
[4]  
RN  
RP  
SEQUENCE FROM N.A.  
RC STRAIN=NOND; TISSUE=Thymus;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."  
RL Genome Res. 10:1617-1630(2000).  
[5]  
RN

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RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kuni H., Akiyama J., Nishi K., Kitsuunai T., Taghiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-Format
RL sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanaoka T., Hara A., Hashizume W.,
RA Hayaehida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saibata K., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akhiba S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC
CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -1- SIMILARITY: Belongs to the thymidylate synthase family.
CC EMBL; AK088134; BAC40165.1; -.
CC HSSP; P45352; 1RTS.
CC MGD; MGI:98878; Tyms.
CC GO; GO:0008168; F:methyltransferase activity; IEA.
CC GO; GO:0004799; F:thymidylate synthase activity; IEA.
CC GO; GO:0016740; F:transferase activity; IEA.
CC GO; GO:0006231; P:dTMP biosynthesis; IEA.
CC GO; GO:0009165; P:nucleotide biosynthesis; IEA.
CC InterPro; IPR000398; Thymidylat synth.
CC PRINTS; PR00108; THYMDSNTHASE.
CC PRODOM; PD001180; Thymidylat synth.
CC PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
KW Methyltransferase; Nucleotide biosynthesis; Transferase.
FT NON TER
FT 1
SQ SEQUENCE 222 AA; 25209 MW; 3E8BDAF742DCC01 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 222;
Best Local Similarity 80.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 104 CHALC 108
|||||

RESULT 78
Q8WYK4 PRELIMINARY; PRT; 230 AA.
AC Q8WYK4
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Thymidylate synthase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22592598; PubMed=12706868; DOI=10.1016/S0304-3835(03)00005-3;

RA Hisatomi H., Tanemura H., Iizuka T., Katsumata K., Nagao K.,
RA Sumida H., Udagawa H., Hikiji K.;
RT "Differential alternative splicing expressions of thymidylate synthase
RT isoforms.";
RL Cancer Lett. 193:127-131(2003).
CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -1- SIMILARITY: Belongs to the thymidylate synthase family.
CC EMBL; AB077207; BAB93676.1; -.
CC HSSP; P04818; 1HYV.
CC GO; GO:0008168; F:methyltransferase activity; IEA.
CC GO; GO:0004799; F:thymidylate synthase activity; IEA.
CC GO; GO:0016740; F:transferase activity; IEA.
CC GO; GO:0006231; P:dTMP biosynthesis; IEA.
CC GO; GO:0009165; P:nucleotide biosynthesis; IEA.
CC Pfam; PF00303; Thymidylat synt.
CC PRINTS; PR00108; THYMDSNTHASE.
CC PRODOM; PD001180; Thymidylat synth.
CC PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
KW Methyltransferase; Nucleotide biosynthesis; Transferase.
SQ SEQUENCE 230 AA; 26140 MW; D09F8316A504A02A CRC64;

Query Match 91.2%; Score 31; DB 2; Length 230;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 112 CHALC 116
|||||

RESULT 79
Q8QNP2 PRELIMINARY; PRT; 232 AA.
AC Q8QNP2
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Esv-1-19.
GN Name=ORF 19;
OS Ectocarpus siliculosus virus.
OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phaeovirus.
OX NCBI_TaxID=37665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Esv-1;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF204951; AAK14445.1; -.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004844; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR000345; CvtC_heme_BS.
DR InterPro; IPR001841; Znf_king.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 232 AA; 26241 MW; 893749786BBB4D3 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 232;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 128 CHAMC 132
|||||

RESULT 80
Q9FYL9 PRELIMINARY; PRT; 251 AA.
AC Q9FYL9
ID Q9FYL9

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DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE F21J9.10 (Hypothetical protein Atlg24440).  
 GN Name=Atlg24440;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim C.,  
 RA Shinn P., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L.,  
 RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,  
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharasy N., Nguyen M.,  
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,  
 RA Toriumi M., Vaysberg M., Yu G., Federspiel N., Theologis A.,  
 RA Ecker J.R.;  
 RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,  
 RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,  
 RA Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,  
 RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharasy N.,  
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,  
 RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,  
 RA Theologis A., Ecker J.;  
 RA Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 RL [3]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=22088475; PubMed=12093376;  
 RA Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,  
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.B.;  
 RA "Full-length messenger RNA sequences greatly improve genome  
 RT annotation";  
 RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
 RA Feldmann K.;  
 RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Huan V.W., Lee J.M.,  
 RA Quach H.L., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,  
 RA Yu G., Yuan S., Chen H., Cheuk R., Jones T., Kim C.J., Nguyen M.,  
 RA Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,  
 RA Ecker J.R., Theologis A.;  
 RA Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC000103; AAF97956.1; -;  
 DR EMBL; AY085533; AAM62757.1; -;  
 DR EMBL; BT000927; AAN41327.1; -;  
 DR PIR; E86378; E86378.  
 DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.  
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.  
 DR GO; GO:0008270; F:protein binding; IEA.  
 DR GO; GO:0016567; F:protein ubiquitination; IEA.  
 DR InterPro; IPR001841; Znf\_ring.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS00518; ZF\_RING\_1; UNKNOWN\_1.  
 DR PROSITE; PS00089; ZF\_RING\_2; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 251 AA; 29487 MW; FCAA26695D467218 CRC64;  
 Query Match 91.2%; Score 31; DB 2; Length 251;  
 Best Local Similarity 80.0%; Pred. No. 5e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CHAVC 5  
 Db 171 CHAVC 175

RESULT 81  
 Q7MU57 PRELIMINARY; PRT; 261 AA.  
 AC Q7MU57;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE MazG family protein.  
 GN OrderedLocusNames=PGL1703;  
 OS Porphyromonas gingivalis (Bacteroides gingivalis).  
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
 OC Porphyromonadaceae; Porphyromonas.  
 OX NCBI\_TaxID=837;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=W83; PubMed=12949112;  
 RX MEDLINE=22829867; PubMed=12949112;  
 RX DOI=10.1128/JB.185.18.5591-5601.2003;  
 RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,  
 RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,  
 RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,  
 RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,  
 RA Dewhirst F.E., Fraser C.M.;  
 RA "Complete genome sequence of the oral pathogenic bacterium  
 RT Porphyromonas gingivalis strain W83";  
 RL J. Bacteriol. 185:5591-5601(2003).  
 DR EMBL; AE017177; AAQ66714.1; -;  
 DR TIGR; PGI703; -;  
 DR InterPro; IPR011029; DEATH\_like.  
 DR InterPro; IPR004518; MazG.  
 DR InterPro; IPR011551; MazG\_bact.  
 DR Pfam; PF03819; MazG; 2.  
 DR TIGRFAMs; TIGR00444; mazG; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 261 AA; 29868 MW; E4720FD02BFF0ABC CRC64;  
 Query Match 91.2%; Score 31; DB 2; Length 261;  
 Best Local Similarity 80.0%; Pred. No. 5.2e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CHAVC 5  
 Db 89 CHAVC 93

RESULT 82  
 Q9VDN1 PRELIMINARY; PRT; 272 AA.  
 AC Q9VDN1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE CG4342-PA.  
 GN ORFNames=CG4342;  
 OS Drosophila melanogaster (Fruit fly).  
 OC Sukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brannon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,



RA Perryman S.M., Rossana C., Deng T., Vanin E.F., Johnson L.F.;  
 RT "Sequence of a cDNA for mouse thymidylate synthase reveals striking  
 RL similarity with the prokaryotic enzyme."; Mol. Biol. Evol. 3:313-321(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87057259; PubMed=3782103;  
 RA Deng T., Li D., Jenh C.-H., Johnson L.F.;  
 RT "Structure of the gene for mouse thymidylate synthase. Locations of  
 RL introns and multiple transcriptional start sites."; J. Biol. Chem. 261:16000-16005(1986).  
 RN [3]  
 RP SEQUENCE OF 236-265 FROM N.A.  
 RX MEDLINE=89128436; PubMed=2915925;  
 RA Deng T., Li Y., Johnson L.F.;  
 RT "Thymidylate synthase gene expression is stimulated by some (but not  
 RL all) introns."; Nucleic Acids Res. 17:645-658(1989).  
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =  
 CC dihydrofolate + dTMP.  
 CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SIMILARITY: Belongs to the thymidylate synthase family.  
 CC -----  
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 CC -----  
 DR EMBL; M13019; AAA40439.1; -.  
 DR EMBL; M13352; AAA40444.1; JOINED.  
 DR EMBL; J02617; AAA40444.1; JOINED.  
 DR EMBL; M13347; AAA40444.1; JOINED.  
 DR EMBL; M13348; AAA40444.1; JOINED.  
 DR EMBL; M13349; AAA40444.1; JOINED.  
 DR EMBL; M13350; AAA40444.1; JOINED.  
 DR EMBL; M13351; AAA40444.1; JOINED.  
 DR EMBL; X14489; CAA32851.1; -.  
 DR PIR; A26323; YXMSI.  
 DR HSSP; P45352; 1RTS.  
 DR MGD; MGI:98878; Tmys.  
 DR InterPro; IPR000398; Thymidylat synth.  
 DR Pfam; PF00303; Thymidylat\_synth; 1.  
 DR PRINTS; PR00108; THYMSDNTHASE.  
 DR ProDom; PD001180; Thymidylat\_synth; 1.  
 DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.  
 KW Methyltransferase; Nucleotide biosynthesis; Transferase.  
 FT ACT SITE 189 By similarity.  
 SQ SEQUENCE 307 AA; 34958 MW; E4930618C487FD5E CRC64;  
 Query Match 91.2%; Score 31; DB 1; Length 307;  
 Best Local Similarity 80.0%; Pred. No. 6.1e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CHAVC 5  
 Db 189 CHALC 193  
 RESULT 85  
 TISY\_RAT  
 ID TISY\_RAT STANDARD; PRT; 307 AA.  
 AC P45352;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Thymidylate synthase (EC 2.1.1.45) (TMSase).  
 GN Name=Tmys;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95226450; PubMed=7711067; DOI=10.1016/0167-4781(95)00008-5;  
 RA Ciesla J., Weiner K.X., Weiner R.S., Reeton J.T., Maley G.F.,  
 RA Maley F.;  
 RT "Isolation and expression of rat thymidylate synthase cDNA:  
 RL phylogenetic comparison with human and mouse thymidylate synthases."; Biochim. Biophys. Acta 1261:233-242(1995).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).  
 RX MEDLINE=99110611; PubMed=9894005; DOI=10.1021/bi981881d;  
 RA Sotelo-Mundo R.R., Ciesla J., Dziak J.M., Rode W., Maley F.,  
 RA Maley G.F., Hardy L.W., Montfort W.R.;  
 RT "Crystal structures of rat thymidylate synthase inhibited by Tomudex,  
 RL a potent anticancer drug."; Biochemistry 38:1087-1094(1999).  
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =  
 CC dihydrofolate + dTMP.  
 CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SIMILARITY: Belongs to the thymidylate synthase family.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; L12138; AAA92340.1; -.  
 DR PIR; S53715; S53715.  
 DR PDB; 1RTS; X-ray; A/B=1-307.  
 DR PDB; 2TSR; X-ray; A/B/C/D=1-307.  
 DR RGD; 3921; Tmys.  
 DR InterPro; IPR000398; Thymidylat synth.  
 DR Pfam; PF00303; Thymidylat\_synth; 1.  
 DR PRINTS; PR00108; THYMSDNTHASE.  
 DR ProDom; PD001180; Thymidylat\_synth; 1.  
 DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.  
 KW 3D-structure; Methyltransferase; Nucleotide biosynthesis; Transferase.  
 FT ACT SITE 189 By similarity.  
 FT TURN 23 23  
 FT TURN 24 37  
 FT HELIX 24 41  
 FT STRAND 39 41  
 FT STRAND 49 60  
 FT TURN 62 63  
 FT TURN 75 86  
 FT HELIX 75 88  
 FT TURN 91 91  
 FT STRAND 91 92  
 FT TURN 92 92  
 FT HELIX 93 96  
 FT TURN 97 99  
 FT TURN 102 104  
 FT TURN 105 107  
 FT HELIX 109 114  
 FT TURN 115 116  
 FT TURN 122 123  
 FT STRAND 124 124  
 FT HELIX 129 134  
 FT STRAND 136 136  
 FT STRAND 137 137  
 FT TURN 143 144  
 FT TURN 148 149  
 FT STRAND 152 152  
 FT HELIX 154 164  
 FT TURN 166 167  
 FT STRAND 172 174  
 FT TURN 178 180  
 FT TURN 181 183  
 FT HELIX 181 198  
 FT STRAND 190 198



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FT TURN 199 200
FT STRAND 201 212
FT TURN 213 215
FT HELIX 216 235
FT TURN 236 236
FT STRAND 238 252
FT HELIX 253 255
FT HELIX 256 264
FT STRAND 272 275
FT HELIX 282 284
FT HELIX 287 289
FT STRAND 290 293
SQ SEQUENCE 307 AA; 159F564D347B2B52 CRC64;

Query Match 91.2%; Score 31; DB 1; Length 307;
Best Local Similarity 80.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 189 CHALC 193

RESULT 86
Q9DOH1 PRELIMINARY; PRT; 307 AA.
AC Q9DOH1
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2610017621 product:thymidylate synthase, full
DE insert sequence.
DE Name=Tyms;
GS Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN RIKEN FANTOM Consortium; DOI=10.1016/S0076-6879(99)03004-9;
RP STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium; DOI=10.1038/35055500;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RN RIKEN FANTOM Consortium; DOI=10.1038/35055500;
RP STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium; DOI=10.1038/35055500;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RN RIKEN FANTOM Consortium; DOI=10.1038/35055500;
RP STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RN RIKEN FANTOM Consortium; DOI=10.1038/35055500;
RP STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

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RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN RIKEN FANTOM Consortium; DOI=10.1038/35055500;
RP STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hangaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -| CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -| PATHWAY: Deoxyribonucleotide biosynthesis.
CC -| SIMILARITY: Belongs to the thymidylate synthase family.
DR EMBL; AK011435; BAB27620.1; -.
DR HSSP; P45352; 1RTS.
DR MGD; MGI:98878; Tyms.
DR GO; GO:0008168; P:methyltransferase activity; IEA.
DR GO; GO:0004799; P:thymidylate synthase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.
DR InterPro; IPR000398; Thymidylat_synth.
DR Pfam; PF00303; Thymidylat_synth; 1.
DR PRINTS; PD00108; THYMDSNTASE.
DR ProDom; PD001180; Thymidylat_synth; 1.
DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
KW Methyltransferase; Nucleotide biosynthesis; Transferase.
SQ SEQUENCE 307 AA; 34989 MW; E4930618C52CE7EE CRC64;

Query Match 91.2%; Score 31; DB 2; Length 307;
Best Local Similarity 80.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 189 CHALC 193

RESULT 87
Q8VDV6 PRELIMINARY; PRT; 307 AA.
AC Q8VDV6
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tyms protein.
GN Name=Tyms;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN RIKEN FANTOM Consortium; DOI=10.1038/35055500;
RP STRAIN=C57BL/6J; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C2ECH II; TISSUE=Mammary tumor;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =  
CC dihydrofolate + dTMP.  
CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.  
CC -1- SIMILARITY: Belongs to the thymidylate synthase family.  
DR EMBL; BC020119; AAH20139.1; --  
DR HSSP; P45352; IRTS.  
DR MGD; MG1:98878; Tyms.  
DR GO; GO:0008168; F:methyltransferase activity; IEA.  
DR GO; GO:0004799; F:thymidylate synthase activity; IEA.  
DR GO; GO:0016740; P:transferase activity; IEA.  
DR GO; GO:0006231; P:dTMP biosynthesis; IEA.  
DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.  
DR Pfam; PF00303; Thymidylat synt; 1.  
DR PRINTS; PR00108; THYMSNTASE.  
DR PRODOM; PD001180; Thymidylat synth; 1.  
DR PROSITE; PS00091; THYIMIDYLATE SYNTHASE; 1.  
KW Methyltransferase; Nucleotide biosynthesis; Transferase.  
SQ SEQUENCE 307 AA; 34930 MW; 76F797162468FD9D CRC64;

Query Match 91.2%; Score 31; DB 2; Length 307;  
Best Local Similarity 80.0%; Pred. No. 6.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
Db 189 CHALC 193

RESULT 88  
ID Q8MQS5 PRELIMINARY; PRT; 310 AA.  
AC Q8MQS5;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE GH05249p (Fragment).  
GN ORFNames=CG4342;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkely;  
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
RA Champe R., Chavez C., Dorsett V., Drensek D., Farfan D., Frise E.,  
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,  
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,  
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

RA Celniker S.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY128415; AAM75008.1; --  
DR FlyBase; FBgn0038791; CG4342.  
FT NON TER 1  
SQ SEQUENCE 310 AA; 34213 MW; 7641F9761512F5CC CRC64;  
Query Match 91.2%; Score 31; DB 2; Length 310;  
Best Local Similarity 80.0%; Pred. No. 6.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
Db 93 CHALC 97

RESULT 89  
ID TYSY\_HUMAN STANDARD; PRT; 312 AA.  
AC P04818;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 25-JAN-2005 (Rel. 46, Last annotation update)  
DE Thymidylate synthase (EC 2.1.1.45) (TS) (Tsase) (OK/SW-cl.29).  
GN Name=TYMS; Synonyms=TS;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85215597; PubMed=2987839;  
RA Takeishi K., Kaneda S., Ayusawa D., Shimizu K., Gotoh O., Seno T.;  
RT "Nucleotide sequence of a functional cDNA for human thymidylate  
RT synthase";  
RL Nucleic Acids Res. 13:2035-2043 (1985).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91056070; PubMed=2243092;  
RA Kaneda S., Nalbantoglu J., Takeishi K., Shimizu K., Gotoh O., Seno T.,  
RA Ayusawa D.;  
RT "Structural and functional analysis of the human thymidylate synthase  
RT gene";  
RL J. Biol. Chem. 265:20277-20284 (1990).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Colon adenocarcinoma;  
RA Shichijo S., Itoh K.;  
RT "Identification of immuno-peptidomics that recognized by tumor-reactive  
RT CTL generated from TIL of colon cancer patients";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow, and Placenta;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,  
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [5]

RP SEQUENCE OF 1-67 FROM N.A.

RA MEDLINE=90110051; PubMed=2532645;

RX Takeishi K., Kaneda S., Ayusawa D., Shimizu K., Gotoh O., Seno T.;

RA "Human thymidylate synthase gene: isolation of phage clones which

RT cover a functionally active gene and structural analysis of the region

RT upstream from the translation initiation codon.";

RL J. Biochem. 106:575-583(1989).

RN [6]

RP SEQUENCE OF 1-24.

RX MEDLINE=85261174; PubMed=3839505;

RA Shimizu K., Ayusawa D., Takeishi K., Seno T.;

RT "Purification and NH2-terminal amino acid sequence of human

RT thymidylate synthase in an overproducing transformant of mouse FM3A

RL cells.";

RN J. Biochem. 97:845-850(1985).

RN [7]

RP SEQUENCE OF 1-9.

RX PubMed=2656695;

RA Davison V.J., Sirawaraporn W., Santi D.V.;

RT "Expression of human thymidylate synthase in *Escherichia coli*.";

RL J. Biol. Chem. 264:9145-9148(1989).

RN [8]

RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).

RX MEDLINE=96110704; PubMed=8845352;

RA Schiffer C.A., Clifton I.J., Davison V.J., Santi D.V., Stroud R.M.;

RT "Crystal structure of human thymidylate synthase: a structural

RT mechanism for guiding substrates into the active site.";

RL Biochemistry 34:16279-16287(1995).

RN [9]

RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

RX MEDLINE=21299106; PubMed=11329255; DOI=10.1021/bi002413i;

RA Phan J., Koli S., Minor W., Dunlap R.B., Berger S.H., Lebioda L.;

RT "Human thymidylate synthase is in the closed conformation when

RT complexed with dUMP and raltitrexed, an antifolate drug.";

RL Biochemistry 40:1897-1902(2001).

RN [10]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RX MEDLINE=21216721; PubMed=11278511; DOI=10.1074/jbc.M009493200;

RA Phan J., Steadman D.J., Koli S., Ding W.C., Minor W., Dunlap R.B.,

RA Berger S.H., Lebioda L.;

RT "Structure of human thymidylate synthase suggests advantages of

RT chemotherapy with noncompetitive inhibitors.";

RL J. Biol. Chem. 276:14170-14177(2001).

CC -I- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =

CC dihydrofolate + dTMP.

CC -I- PATHWAY: Deoxyribonucleotide biosynthesis.

CC -I- SUBUNIT: Homodimer.

CC -I- SIMILARITY: Belongs to the thymidylate synthase family.

CC -----

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CC the European Bioinformatics Institute. There are no restrictions on its

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

CC EMBL: X02308; CAA26178.1; -

DR ENBL: D00596; BAA00472.1; -

DR ENBL: AB062290; BAB93473.1; -

DR ENBL: BC002567; AAH02567.1; -

DR ENBL: BC013919; AAH13919.1; -

DR ENBL: D00517; BAA00404.1; -

DR PIR: A23047; YXHUT.

DR PDB: 1HWY; X-ray; A/B/C/D=25-312.

DR PDB: 1HW3; X-ray; A=1-312.

DR PDB: 1HW4; X-ray; A=1-312.

DR PDB: 1HW2; X-ray; A/B=23-312.

DR PDB: 1I00; X-ray; A/B=23-312.

DR PDB: 1JU6; X-ray; A/B/C/D=1-312.

DR PDB: 1JUJ; X-ray; A/B/C/D=1-312.

DR Genew: HGNC:12441; TYMS.

DR H-InvDB: HIX0017793; -

DR Reactome: P04818; -

DR MIM: 188350; -

DR GO: GO:0009157; P:deoxyribonucleoside monophosphate biosynthesis; TAS.

DR GO: GO:0006139; P:nucleobase, nucleoside, nucleotide and nucl. . .; TAS.

DR InterPro: IPR000398; Thymidylat synth.

DR Pfam: PF00303; Thymidylat synt; 1.

DR PRINTS: PRO0108; THYMDSNTASE.

DR ProDom: PD001180; Thymidylat synth; 1.

DR PROSITE: PS00091; THYMIDYLATE SYNTHASE; 1.

KW 3D-structure; Direct protein sequencing; Methyltransferase;

KW Nucleotide biosynthesis; Transferase.

FT INIT\_MET 0

FT ACT\_SITE 194 194

FT TURN 28 28

FT HELIX 29 42

FT STRAND 44 46

FT TURN 49 50

FT STRAND 54 65

FT TURN 67 68

FT TURN 74 77

FT HELIX 80 91

FT TURN 92 93

FT STRAND 96 96

FT HELIX 97 101

FT TURN 102 104

FT TURN 107 109

FT HELIX 110 112

FT HELIX 114 119

FT TURN 120 121

FT TURN 123 124

FT TURN 127 128

FT STRAND 129 129

FT HELIX 134 140

FT STRAND 141 141

FT TURN 142 142

FT TURN 148 149

FT TURN 153 154

FT STRAND 157 157

FT HELIX 159 169

FT TURN 171 172

FT TURN 174 175

FT STRAND 177 179

FT TURN 183 185

FT HELIX 186 188

FT STRAND 195 203

FT TURN 204 205

FT STRAND 206 217

FT TURN 218 220

FT HELIX 221 239

FT STRAND 240 241

FT STRAND 243 257

FT HELIX 258 260

FT HELIX 261 268

FT TURN 269 269

FT STRAND 277 280

FT HELIX 287 289

FT STRAND 292 294

FT TURN 295 298

SQ SEQUENCE 312 AA; A66F056D1973AB41 CRC64;

Query Match 91.2%; Score 31; DB 1; Length 312;

Best Local Similarity 80.0%; Pred. No. 6.2e-02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5

DB 194 CHAC 198

RESULT 90

Q6P045 PRELIMINARY; PRT; 318 AA.  
 ID Q6P045;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Zgc:56465 protein.  
 GN Name=zgc:56465; ORFNames=zgc:77659;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole;  
 RX Strausberg R.;  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =  
 dihydrofolate + dTMP.  
 CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.  
 CC -1- SIMILARITY: Belongs to the thymidylate synthase family.  
 DR EMBL; BC065845; AAH65845.1; -.  
 DR ZFIN; ZDB-GENE-040426-60; zgc:77659.  
 DR GO; GO:0008168; F:methyltransferase activity; IEA.  
 DR GO; GO:0004799; F:thymidylate synthase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006231; P:dTMP biosynthesis; IEA.  
 DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.  
 DR InterPro; IPR000398; Thymidylat\_synth.  
 DR PRINTS; PR00108; THYMSNTHASE.  
 DR PRODOM; PD001180; Thymidylat synth; 1.  
 DR PROSITE; PS00091; THYMDYLATE SYNTHASE; 1.  
 KW Methyltransferase; Nucleotide biosynthesis; Transferase.  
 SQ SEQUENCE 318 AA; 36183 MW; 47E9BABA24927372 CRC64;  
 Query Match 91.2%; Score 31; DB 2; Length 318;  
 Best Local Similarity 80.0%; Pred. No. 6.3e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CHAVC 5  
 DB 200 CHALC 204  
 RESULT 91  
 Q7ZUI7 PRELIMINARY; PRT; 319 AA.  
 ID Q7ZUI7

Q7ZUI7;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Tyms protein.  
 GN ORFNames=zgc:56465;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole body;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Brownstein M.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole body;  
 RX Strausberg R.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =  
 dihydrofolate + dTMP.  
 CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.  
 CC -1- SIMILARITY: Belongs to the thymidylate synthase family.  
 DR EMBL; BC049026; AAH49026.1; -.  
 DR HSSP; P04818; 1HW4.  
 DR ZFIN; ZDB-GENE-040426-59; zgc:56465.  
 DR GO; GO:0008168; F:methyltransferase activity; IEA.  
 DR GO; GO:0004799; F:thymidylate synthase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006231; P:dTMP biosynthesis; IEA.  
 DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.  
 DR InterPro; IPR000398; Thymidylat\_synth.  
 DR Pfam; PF00303; thymidylat\_synth; 1.  
 DR PRINTS; PR00108; THYMSNTHASE.  
 DR PRODOM; PD001180; Thymidylat synth; 1.  
 DR PROSITE; PS00091; THYMDYLATE SYNTHASE; 1.  
 KW Methyltransferase; Nucleotide biosynthesis; Transferase.  
 SQ SEQUENCE 319 AA; 36299 MW; ADFA451E1DDF891A CRC64;  
 Query Match 91.2%; Score 31; DB 2; Length 319;  
 Best Local Similarity 80.0%; Pred. No. 6.3e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CHAVC 5  
 DB 201 CHALC 205  
 RESULT 92  
 Q9DGH5 PRELIMINARY; PRT; 319 AA.  
 ID Q9DGH5  
 AC Q9DGH5;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Thymidylate synthase.  
 GN ORFNames=zgc:56465;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Gill R.L., Jr., Warren J.T. Jr.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =  
 CC dihydrofolate + dTMP.  
 CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.  
 CC -1- SIMILARITY: Belongs to the thymidylate synthase family.  
 DR EMBL; AY005904; AAF97476.1; -.  
 DR HSSP; P04818; 1HW4.  
 DR ZFIN; ZDB-GENE-040426-59; ZGC:56465.  
 DR GO; GO:0008168; F:methyltransferase activity; IEA.  
 DR GO; GO:0004799; F:thymidylate synthase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006231; P:dTMP biosynthesis; IEA.  
 DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.  
 DR InterPro; IPR000398; Thymidylat\_synth.  
 DR Pfam; PF00303; Thymidylat\_synth.  
 DR PRINTS; PR00108; THYMDNSTHASE.  
 DR ProDom; PD001180; Thymidylat synth; 1.  
 DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.  
 KW Methyltransferase; Nucleotide\_biosynthesis; Transferase.  
 SQ SEQUENCE 319 AA; 36313 MW; E08B155B09DE1E84 CRC64;  
  
 Query Match 91.2%; Score 31; DB 2; Length 319;  
 Best Local Similarity 80.0%; Pred. No. 6.3e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 CHAVC 5  
 DB 201 CHALC 205  
  
 RESULT 93  
 ID P91501 PRELIMINARY; PRT; 373 AA.  
 AC P91501;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein T27A3.7;  
 GN Names=T27A3.7; ORFNames=T27A3.7;  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RG WormBase Consortium;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology. The C. elegans Sequencing Consortium.";  
 RL Science 282:1202-1208 (1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Murray J., Wohldmann P.;  
 RT "The sequence of C. elegans cosmid T27A3.";  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;

RA Waterston R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Wilson R.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RG WormBase Consortium;  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U88180; AAB42300.1; -.  
 DR PIR; T25920; T25920.  
 DR WormBase; WBGene0020843; T27A3.7.  
 DR WormPep; T27A3.7; CE14229.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 DR InterPro; IPR000345; Cytochrome BS.  
 DR InterPro; IPR002219; DAG PE-bind.  
 DR InterPro; IPR011011; FYVE\_PHD\_ZnF.  
 DR SMART; SM00109; C1; 1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 373 AA; 42560 MW; F5DDFEFC9FCF29B9 CRC64;  
  
 Query Match 91.2%; Score 31; DB 2; Length 373;  
 Best Local Similarity 80.0%; Pred. No. 7.3e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 CHAVC 5  
 DB 262 CHALC 266  
  
 RESULT 94  
 ID Q8EED1 PRELIMINARY; PRT; 380 AA.  
 AC Q8EED1;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein SO2451.  
 GN OrderedLocustNames=SO2451;  
 OS Shewanella oneidensis.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;  
 OC Shewanellaceae; Shewanella.  
 OX NCBI\_TaxID=70863;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MR-1;  
 RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;  
 RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,  
 RA Read T.D., Eisen J.A., Seshadri R., Ward N.B., Methe B.A.,  
 RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,  
 RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,  
 RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,  
 RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Imbram M.,  
 RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,  
 RA Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,  
 RA Venter J.C., Neale K.H., Fraser C.M.;  
 RT "Genome sequence of the dissimilatory metal ion-reducing bacterium  
 RT Shewanella oneidensis.";  
 RL Nat. Biotechnol. 20:1118-1123 (2002).  
 DR EMBL; AE015686; AAN55485.1; -.  
 DR TIGR; SO2451; -.  
 KW Complete proteome.  
 SQ SEQUENCE 380 AA; 42539 MW; 562E0C3E60B5CF0F CRC64;  
  
 Query Match 91.2%; Score 31; DB 2; Length 380;  
 Best Local Similarity 80.0%; Pred. No. 7.4e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 CHAVC 5



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Db          73 CHALC 77

RESULT 98
Q8X0Q2      PRELIMINARY;      PRT;      447 AA.
AC Q8X0Q2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Related to 60S ribosomal protein L2 (Mitochondrial).
GN Name=SE6.150;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; AL670004; CAD21256.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR Pfam; PF01016; Ribosomal L27; 1.
DR PRINTS; PR00063; RIBOSOMALL27.
DR ProDom; PD00114; Ribosomal_L27; 1.
KW Ribosomal protein.
SQ SEQUENCE 447 AA; 49442 MW; 404A02A606F613D4 CRC64;

Query Match          91.2%; Score 31; DB 2; Length 447;
Best Local Similarity 80.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 CHAVC 5
           |||:|
Db          18 CHSVC 22

RESULT 99
Q89GP2      PRELIMINARY;      PRT;      481 AA.
AC Q89GP2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE B116303 protein.
GN OrderedLocustNames=b116303;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA110.
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiyama T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpō S., Teurloka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110."
RL DNA Res. 9:189-197(2002).
DR EMBL; AF005958; BAC51568.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.
DR InterPro; IPR002797; PolySacc_synt.
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DR Pfam; PF01943; PolySacc_synt; 1.
KW Complete proteome.
SQ SEQUENCE 481 AA; 52048 MW; CAD37FB12B1B34D8 CRC64;

Query Match          91.2%; Score 31; DB 2; Length 481;
Best Local Similarity 80.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 CHAVC 5
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Db          389 CHALC 393

RESULT 100
Q7QDE4      PRELIMINARY;      PRT;      502 AA.
AC Q7QDE4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AGCF10190.
GN Name=agCG47224; ORFNames=ENSANGG00000011737;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB0100851; EAA07305.1; -.
SQ SEQUENCE 502 AA; 55977 MW; 89AC334BCE3B2E8C CRC64;

Query Match          91.2%; Score 31; DB 2; Length 502;
Best Local Similarity 80.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 CHAVC 5
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Db          276 CHALC 280

Search completed: July 27, 2005, 00:01:04
Job time : 178 secs
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OM protein - protein search, using sw model

Run on: July 27, 2005, 00:01:11 ; Search time 157 Seconds  
(without alignments)  
12.388 Million cell updates/sec

Title: US-10-632-678-10

Perfect score: 34

Sequence: 1 CHAVC 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 38892284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/PCT NEW PUB.pdb.\*

2: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pdb.\*

3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW PUB.pdb.\*

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6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pdb.\*

7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW PUB.pdb.\*

8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pdb.\*

9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pdb.\*

10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pdb.\*

11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pdb.\*

12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW PUB.pdb.\*

13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pdb.\*

14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pdb.\*

15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pdb.\*

16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pdb.\*

17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pdb.\*

18: /cgn2\_6/ptodata/2/pubpaa/US10F\_NEW PUB.pdb.\*

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20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW PUB.pdb.\*

21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW PUB.pdb.\*

22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	34	100.0	5	US-09-234-395-296
2	34	100.0	5	US-09-305-928-296
3	34	100.0	5	US-09-769-145-10
4	34	100.0	5	US-10-006-982-8
5	34	100.0	5	US-10-105-008-96
6	34	100.0	5	US-10-058-821-10
7	34	100.0	5	US-10-359-546-10
8	34	100.0	5	US-10-369-226-32
9	34	100.0	5	US-10-369-226-34
10	34	100.0	5	US-10-425-557-10
11	34	100.0	5	US-10-412-701-10
12	34	100.0	5	US-10-632-678-10
13	34	100.0	5	US-10-759-379-296
14	34	100.0	5	US-10-759-507-296
15	34	100.0	5	US-10-836-289-20
16	34	100.0	6	US-09-769-145-81
17	34	100.0	6	US-09-769-145-84
18	34	100.0	6	US-09-769-145-85
19	34	100.0	6	US-09-769-145-88
20	34	100.0	6	US-09-769-145-89
21	34	100.0	6	US-09-769-145-90
22	34	100.0	6	US-10-105-008-10
23	34	100.0	6	US-10-105-008-84
24	34	100.0	6	US-10-105-008-87
25	34	100.0	6	US-10-105-008-88
26	34	100.0	6	US-10-105-008-91
27	34	100.0	6	US-10-105-008-92
28	34	100.0	6	US-10-105-008-93
29	34	100.0	6	US-10-105-008-95
30	34	100.0	6	US-10-425-557-81
31	34	100.0	6	US-10-425-557-84
32	34	100.0	6	US-10-425-557-85
33	34	100.0	6	US-10-425-557-88
34	34	100.0	6	US-10-425-557-89
35	34	100.0	6	US-10-425-557-90
36	34	100.0	6	US-10-412-701-81
37	34	100.0	6	US-10-412-701-84
38	34	100.0	6	US-10-412-701-85
39	34	100.0	6	US-10-412-701-88
40	34	100.0	6	US-10-412-701-89
41	34	100.0	6	US-10-412-701-90
42	34	100.0	6	US-10-632-678-84
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49	34	100.0	7	US-09-769-145-86
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53	34	100.0	7	US-10-425-557-86
54	34	100.0	7	US-10-425-557-87
55	34	100.0	7	US-10-412-701-86
56	34	100.0	7	US-10-412-701-87
57	34	100.0	7	US-10-632-678-89
58	34	100.0	7	US-10-632-678-90
59	34	100.0	7	US-10-632-678-96
60	34	100.0	8	US-10-632-678-95
61	34	100.0	8	US-09-769-145-86
62	34	100.0	42	US-09-769-145-87
63	34	100.0	62	US-10-424-599-172220
64	34	100.0	62	US-10-437-963-133433
65	34	100.0	110	US-10-425-115-323830
66	34	100.0	121	US-10-291-172-630
67	34	100.0	121	US-10-421-478-630
68	34	100.0	210	US-10-437-963-196854
69	34	100.0	380	US-10-003-806-8
70	34	100.0	382	US-10-437-963-137415
71	34	100.0	424	US-10-437-963-151715
72	34	100.0	513	US-10-437-963-197235
73	34	100.0	537	US-10-047-542-74
74	33	97.1	76	US-10-425-115-315958
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76	33	97.1	102	US-10-437-963-159565
77	33	97.1	110	US-10-424-599-167243
78	33	97.1	241	US-10-424-599-233727
79	33	97.1	242	US-10-424-599-276468
80	33	97.1	243	US-10-424-599-233725
81	33	97.1	280	US-10-437-963-178188
82	33	97.1	314	US-10-425-114-71839
83	33	97.1	343	US-10-437-963-190370
84	33	97.1	426	US-10-437-963-190970
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Sequence 196854,  
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Sequence 71839, A  
Sequence 190970,  
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Sequence 122755,



85 33 97.1 777 16 US-10-437-963-169219 Sequence 169219,  
86 33 97.1 892 16 US-10-437-963-201319 Sequence 201319,  
87 33 97.1 913 16 US-10-437-963-187899 Sequence 187899,  
88 33 97.1 946 16 US-10-437-963-188555 Sequence 188555,  
89 31 91.2 18 16 US-10-629-313-146 Sequence 146, App  
90 31 91.2 18 16 US-10-629-313-150 Sequence 150, App  
91 31 91.2 20 9 US-09-864-761-35523 Sequence 35523, A  
92 31 91.2 49 16 US-10-437-963-174571 Sequence 174571,  
93 31 91.2 51 16 US-10-425-115-211467 Sequence 211467,  
94 31 91.2 55 15 US-10-424-599-163830 Sequence 163830, A  
95 31 91.2 63 9 US-09-864-761-34873 Sequence 34873, A  
96 31 91.2 67 15 US-10-424-599-190876 Sequence 190876,  
97 31 91.2 96 15 US-10-291-265-762 Sequence 762, App  
98 31 91.2 96 16 US-10-425-115-201825 Sequence 201825,  
99 31 91.2 98 16 US-10-437-963-118366 Sequence 118366,  
100 31 91.2 100 15 US-10-424-599-183087 Sequence 183087,

## ALIGNMENTS

## RESULT 1

US-09-234-395-296

; Sequence 296, Application US/09234395

; Patent No. US2002012304A1

; GENERAL INFORMATION:

; APPLICANT: Blaschuk, Orest W.

; APPLICANT: Byers, Stephen

; APPLICANT: Gour, Barbara J.

; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER

; FILE REFERENCE: 100086.407C2

; CURRENT APPLICATION NUMBER: US/09/234,395

; CURRENT FILING DATE: 1999-01-20

; NUMBER OF SEQ ID NOS: 324

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 296

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Product of

; OTHER INFORMATION: Synthesis and Cyclization based on Human

; OTHER INFORMATION: N-Cadherin

; FEATURE:

; OTHER INFORMATION: Cyclic Peptide

US-09-234-395-296

Query Match 100.0%; Score 34; DB 9; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5

Db 1 CHAVC 5

## RESULT 2

US-09-305-928-296

; Sequence 296, Application US/09305928

; Patent No. US20020146687A1

; GENERAL INFORMATION:

; APPLICANT: Blaschuk, Orest W.

; APPLICANT: Byers, Stephen

; APPLICANT: Gour, Barbara J.

; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER

; FILE REFERENCE: 100086.407C4

; CURRENT APPLICATION NUMBER: US/09/305,928

; CURRENT FILING DATE: 1999-05-05

; NUMBER OF SEQ ID NOS: 324

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 296

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Product of  
; OTHER INFORMATION: Synthesis and Cyclization based on Human  
; OTHER INFORMATION: N-Cadherin  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide  
US-09-305-928-296

Query Match 100.0%; Score 34; DB 9; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5

Db 1 CHAVC 5

## RESULT 3

US-09-769-145-10

; Sequence 10, Application US/09769145

; Patent No. US20020168761A1

; GENERAL INFORMATION:

; APPLICANT: Gour, Barbara J.

; APPLICANT: Blaschuk, Orest W.

; APPLICANT: Ali, Ammar

; APPLICANT: Ni, Feng

; APPLICANT: Chen, Zhigang

; APPLICANT: Michaud, Stephanie

; APPLICANT: Wang, Shoameng

; APPLICANT: Hu, Zengjian

; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION

; FILE REFERENCE: 100086.413C1

; CURRENT APPLICATION NUMBER: US/09/769,145

; CURRENT FILING DATE: 2001-01-24

; PRIOR APPLICATION NUMBER: US 09/491,078

; PRIOR FILING DATE: 2000-01-24

; NUMBER OF SEQ ID NOS: 96

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 10

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide

; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence

; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal

; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group

; OTHER INFORMATION: and/or C-terminal modifications such as amide or

; OTHER INFORMATION: ester group

US-09-769-145-10

Query Match 100.0%; Score 34; DB 9; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5

Db 1 CHAVC 5

## RESULT 4

US-10-006-982-8

; Sequence 8, Application US/10006982

; Publication No. US20020151475A1

; GENERAL INFORMATION:

; APPLICANT: Blaschuk, Orest W.

; APPLICANT: Gour, Barbara J.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING

; NUMBER OF SEQUENCES: 47

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED IP LAW GROUP PLLC



STREET: 6300 Bank of America Bldg., 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/006,982

FILING DATE: 04-Dec-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Christiansen, William T.

REGISTRATION NUMBER: 44,614

REFERENCE/DOCKET NUMBER: 100086.401C11

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: circular

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-10-006-982-8

Query Match 100.0%; Score 34; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 1 CHAVC 5

## RESULT 5

US-10-105-008-96

Sequence 96, Application US/10105008

Publication No. US20030065136A1

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Gour, Barbara J.

APPLICANT: Farookhi, Riaz

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION

FILE REFERENCE: 100086.401D1

CURRENT APPLICATION NUMBER: US/10/105,008

CURRENT FILING DATE: 2002-03-22

NUMBER OF SEQ ID NOS: 99

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 96

LENGTH: 5

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide

OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence

OTHER INFORMATION: Cyclic Peptide may comprise N-terminal

OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group

OTHER INFORMATION: and/or C-terminal modifications such as amide or

OTHER INFORMATION: ester group

US-10-105-008-96

Query Match 100.0%; Score 34; DB 14; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 1 CHAVC 5

Db 1 CHAVC 5

## RESULT 6

US-10-058-821-10

Sequence 10, Application US/10058821

Publication No. US20030087811A1

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Gour, Barbara J.

APPLICANT: Farookhi, Riaz

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR CANCER THERAPY

FILE REFERENCE: 100086.401C12

CURRENT APPLICATION NUMBER: US/10/058,821

CURRENT FILING DATE: 2002-01-29

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 10

LENGTH: 5

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide

OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence

OTHER INFORMATION: Cyclic Peptide may comprise N-terminal

OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group

OTHER INFORMATION: and/or C-terminal modifications such as amide or

OTHER INFORMATION: ester group

US-10-058-821-10

Query Match 100.0%; Score 34; DB 14; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 1 CHAVC 5

## RESULT 7

US-10-359-546-10

Sequence 10, Application US/10359546

Publication No. US20030224978A1

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Gour, Barbara J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING APOPTOSIS

FILE REFERENCE: 100086.401C15

CURRENT APPLICATION NUMBER: US/10/359,546

CURRENT FILING DATE: 2003-02-04

NUMBER OF SEQ ID NOS: 81

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 10

LENGTH: 5

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide

OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence

OTHER INFORMATION: Cyclic Peptide may comprise N-terminal

OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group

OTHER INFORMATION: and/or C-terminal modifications such as amide or

OTHER INFORMATION: ester group

US-10-359-546-10

Query Match 100.0%; Score 34; DB 15; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 1 CHAVC 5

Db 1 CHAVC 5

RESULT 8

US-10-369-226-22

Sequence 22, Application US/10369226

Publication No. US20030236186A1

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

Gour, Barbara J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE INTERACTION BETWEEN ALPHA-CATENIN AND BETA-CATENIN

NUMBER OF SEQUENCES: 73

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed Intellectual Property Law Group

STREET: 701 Fifth Avenue, Suite 6300

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/369,226

FILING DATE: 13-Feb-2003

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Christiansen, William T.

REGISTRATION NUMBER: 44,614

REFERENCE/DOCKET NUMBER: 100086.406C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 22:

US-10-369-226-22

Query Match 100.0%; Score 34; DB 15; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 1 CHAVC 5

RESULT 9

US-10-369-226-34

Sequence 34, Application US/10369226

Publication No. US20030236186A1

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

Gour, Barbara J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE INTERACTION BETWEEN ALPHA-CATENIN AND BETA-CATENIN

NUMBER OF SEQUENCES: 73

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed Intellectual Property Law Group

STREET: 701 Fifth Avenue, Suite 6300

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/369,226

FILING DATE: 13-Feb-2003

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Christiansen, William T.

REGISTRATION NUMBER: 44,614

REFERENCE/DOCKET NUMBER: 100086.406C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 22:

US-10-369-226-22

Query Match 100.0%; Score 34; DB 15; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 1 CHAVC 5

RESULT 10

US-10-425-557-10

Sequence 10, Application US/10425557

Publication No. US20040006011A1

GENERAL INFORMATION:

APPLICANT: Gour, Barbara J.

APPLICANT: Blaschuk, Orest W.

APPLICANT: Ali, Ammar

APPLICANT: Ni, Feng

APPLICANT: Chen, Zhigang

APPLICANT: Michaud, Stephanie Denise

APPLICANT: Wang, Shaomeng

APPLICANT: Hu, Zenjian

TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION

FILE REFERENCE: 100086.401C16

CURRENT APPLICATION NUMBER: US/10/425,557

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 10

LENGTH: 5

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide

OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence

FEATURE:

OTHER INFORMATION: Cyclic Peptide may comprise N-terminal

OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group

OTHER INFORMATION: and/or C-terminal modifications such as amide or

OTHER INFORMATION: ester group

US-10-425-557-10

Query Match 100.0%; Score 34; DB 15; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 1 CHAVC 5

```
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 CHAVC 5  
|||  
db 1 CHAVC 5

## RESULT 13

```

US-10-759-379-296
; Sequence 296, Application US/10759379
; Publication No. US20040248219A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER
; FILE REFERENCE: 100086.407C12
; CURRENT APPLICATION NUMBER: US/10759,379
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: 09/305,928
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: 09/234,395
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 09/187,859
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/073,040
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 296
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product
; OTHER INFORMATION: Synthesis and Cyclization based on Human
; OTHER INFORMATION: N-Cadherin
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
; US-10-759-379-296

```

Query Match 100.0%; Score 34; DB 16; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||||

rb 1 CHAVC 5

## RESIT.T 14

```

> US-10-759-507-296
> Sequence 296, Application US/10759507
> Publication No. US20040248220A1
> GENERAL INFORMATION:
> APPLICANT: Blaschuk, Orest W.
> APPLICANT: Symonds, James Matthew
> APPLICANT: Byers, Stephen
> APPLICANT: Gour, Barbara J.
> TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER
> FILE REFERENCE: 100086.407C11
> CURRENT APPLICATION NUMBER: US/10/759,507
> CURRENT FILING DATE: 2004-01-16
> PRIOR APPLICATION NUMBER: 03/234,395
> PRIOR FILING DATE: 1999-01-20
> PRIOR APPLICATION NUMBER: 03/187,859
> PRIOR FILING DATE: 1998-11-06
> PRIOR APPLICATION NUMBER: 09/073,040
> PRIOR FILING DATE: 1998-05-05
> NUMBER OF SEQ ID NOS: 324
> SOFTWARE: PatentIn Ver. 2.0

```

Query Match 100.0%; Score 34; DB 16; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Qy 1 CHAVC 5  
|||||

rb 1 CHAVC 5

## RESULT 11

```

US-10-412-701-10
; Sequence 10, Application US/10412701
; Publication No. US20040058864A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Ammar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, ShaoMeng
; APPLICANT: Hu, ZengJian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.413C2
; CURRENT APPLICATION NUMBER: US/10/412,701
; CURRENT FILING DATE: 2003-04-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic
; OTHER INFORMATION: with Classical Cell Adhesion Recognition S
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl
; OTHER INFORMATION: and/or C-terminal modifications such as am
; OTHER INFORMATION: ester group
US-10-412-701-10

```

Query Match	100.0%	Score 34;	DB 15;	Length 5;
Best Local Similarity	100.0%	Pred. No. 1.6e+06;		

Qy 1 CHAVC 5  
|||||

nb 1 CHAVC 5

```

RESULT 12
US-10-632-678-10
; Sequence 10, Application US/10632678
; Publication No. US20040106545A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 10086.401C18
; CURRENT APPLICATION NUMBER: US/10/632,678
; CURRENT FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-632-678-10

```

Query Match 100.0%; Score 34; DB 16; Length 5;

: SOFTWARE: PatentIn Ver. 2.0

```
; SEQ ID NO 296
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Synthesis and Cyclization based on Human
; OTHER INFORMATION: N-Cadherin
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-10-759-507-296

Query Match          100.0%; Score 34; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      1 CHAVC 5
|||||

RESULT 15
US-10-836-289-20
; Sequence 20, Application US/10836289
; Publication No. US2005004013A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: FRIEDLANDER, Martin
; APPLICANT: DORRELL, Michael. I.
; TITLE OF INVENTION: SELECTIVE R-CADHERIN ANTAGONISTS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: TSRI-987.1
; CURRENT APPLICATION NUMBER: US/10/836,289
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/467,188
; PRIOR FILING DATE: 2003-05-01
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CYCLIC CADHERIN ANTAGONIST, DISULFIDE BOND BETWEEN
; OTHER INFORMATION: Cys1 and Cys5
US-10-836-289-20

Query Match          100.0%; Score 34; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      1 CHAVC 5
|||||

RESULT 16
US-09-769-145-81
; Sequence 81, Application US/09769145
; Patent No. US20020168761A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.413C1
; CURRENT APPLICATION NUMBER: US/09/769,145
; CURRENT FILING DATE: 2001-01-24
```

```
; PRIOR APPLICATION NUMBER: US 09/491,078
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-769-145-81

Query Match          100.0%; Score 34; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      1 CHAVC 5
|||||

RESULT 17
US-09-769-145-84
; Sequence 84, Application US/09769145
; Patent No. US20020168761A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.413C1
; CURRENT APPLICATION NUMBER: US/09/769,145
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 09/491,078
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-769-145-84

Query Match          100.0%; Score 34; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      1 CHAVC 5
|||||

RESULT 18
US-09-769-145-85
; Sequence 85, Application US/09769145
; Patent No. US20020168761A1
```

GENERAL INFORMATION:  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Ali, Anmar  
; APPLICANT: Ni, Feng  
; APPLICANT: Chen, Zhigang  
; APPLICANT: Michaud, Stephanie  
; APPLICANT: Wang, Shoameng  
; APPLICANT: Hu, Zengjian  
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION  
; FILE REFERENCE: 10086.413C1  
; CURRENT APPLICATION NUMBER: US/09/769,145  
; CURRENT FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: US 09/491,078  
; PRIOR FILING DATE: 2000-01-24  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 85  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-09-769-145-85  
Query Match 100.0%; Score 34; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CHAVC 5  
Db 2 CHAVC 6  
RESULT 19  
US-09-769-145-88  
; Sequence 88, Application US/09769145  
; Patent No. US20020168761A1  
; GENERAL INFORMATION:  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Ali, Anmar  
; APPLICANT: Ni, Feng  
; APPLICANT: Chen, Zhigang  
; APPLICANT: Michaud, Stephanie  
; APPLICANT: Wang, Shoameng  
; APPLICANT: Hu, Zengjian  
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION  
; FILE REFERENCE: 10086.413C1  
; CURRENT APPLICATION NUMBER: US/09/769,145  
; CURRENT FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: US 09/491,078  
; PRIOR FILING DATE: 2000-01-24  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 88  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-09-769-145-88

Query Match 100.0%; Score 34; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CHAVC 5  
Db 1 CHAVC 5  
RESULT 20  
US-09-769-145-89  
; Sequence 89, Application US/09769145  
; Patent No. US20020168761A1  
; GENERAL INFORMATION:  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Ali, Anmar  
; APPLICANT: Ni, Feng  
; APPLICANT: Chen, Zhigang  
; APPLICANT: Michaud, Stephanie  
; APPLICANT: Wang, Shoameng  
; APPLICANT: Hu, Zengjian  
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION  
; FILE REFERENCE: 10086.413C1  
; CURRENT APPLICATION NUMBER: US/09/769,145  
; CURRENT FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: US 09/491,078  
; PRIOR FILING DATE: 2000-01-24  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 89  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-09-769-145-89  
Query Match 100.0%; Score 34; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CHAVC 5  
Db 1 CHAVC 5  
RESULT 21  
US-09-769-145-90  
; Sequence 90, Application US/09769145  
; Patent No. US20020168761A1  
; GENERAL INFORMATION:  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Ali, Anmar  
; APPLICANT: Ni, Feng  
; APPLICANT: Chen, Zhigang  
; APPLICANT: Michaud, Stephanie  
; APPLICANT: Wang, Shoameng  
; APPLICANT: Hu, Zengjian  
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION  
; FILE REFERENCE: 10086.413C1  
; CURRENT APPLICATION NUMBER: US/09/769,145  
; CURRENT FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: US 09/491,078  
; PRIOR FILING DATE: 2000-01-24  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 90  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-09-769-145-90

Query Match 100.0%; Score 34; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
|||||  
Db 1 CHAVC 5

## RESULT 22

US-10-105-008-10  
; Sequence 10, Application US/10105008  
; Publication No. US20030065136A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Annar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401D1  
; CURRENT APPLICATION NUMBER: US/10/105,008  
; CURRENT FILING DATE: 2002-03-22  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-10-105-008-10

Query Match 100.0%; Score 34; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
|||||  
Db 2 CHAVC 6

## RESULT 23

US-10-105-008-84  
; Sequence 84, Application US/10105008  
; Publication No. US20030065136A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Annar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401D1  
; CURRENT APPLICATION NUMBER: US/10/105,008  
; CURRENT FILING DATE: 2002-03-22  
; NUMBER OF SEQ ID NOS: 99

; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 84  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-10-105-008-84

Query Match 100.0%; Score 34; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
|||||  
Db 1 CHAVC 5

## RESULT 24

US-10-105-008-87  
; Sequence 87, Application US/10105008  
; Publication No. US20030065136A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Annar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401D1  
; CURRENT APPLICATION NUMBER: US/10/105,008  
; CURRENT FILING DATE: 2002-03-22  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 87  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-10-105-008-87

Query Match 100.0%; Score 34; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
|||||  
Db 1 CHAVC 5

## RESULT 25

US-10-105-008-88  
; Sequence 88, Application US/10105008  
; Publication No. US20030065136A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Annar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401D1  
; CURRENT APPLICATION NUMBER: US/10/105,008  
; CURRENT FILING DATE: 2002-03-22

; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 88  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-10-105-008-88

Query Match 100.0%; Score 34; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CHAVC 5  
|  
|  
|  
|  
|  
Db 2 CHAVC 6  
|  
|  
|  
|  
|

## RESULT 26

US-10-105-008-91  
; Sequence 91, Application US/10105008  
; Publication No. US20030065136A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Ammar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401D1  
; CURRENT APPLICATION NUMBER: US/10/105.008  
; CURRENT FILING DATE: 2002-03-22  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 91  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-10-105-008-91

Query Match 100.0%; Score 34; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CHAVC 5  
|  
|  
|  
|  
|  
Db 1 CHAVC 5  
|  
|  
|  
|  
|

## RESULT 27

US-10-105-008-92  
; Sequence 92, Application US/10105008  
; Publication No. US20030065136A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Ammar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401D1  
; CURRENT APPLICATION NUMBER: US/10/105.008

; CURRENT FILING DATE: 2002-03-22  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 92  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-10-105-008-92

Query Match 100.0%; Score 34; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CHAVC 5  
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|  
|  
|  
Db 1 CHAVC 5  
|  
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|  
|  
|

## RESULT 28

US-10-105-008-93  
; Sequence 93, Application US/10105008  
; Publication No. US20030065136A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Ammar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401D1  
; CURRENT APPLICATION NUMBER: US/10/105.008  
; CURRENT FILING DATE: 2002-03-22  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 93  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-10-105-008-93

Query Match 100.0%; Score 34; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CHAVC 5  
|  
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|  
|  
|  
Db 1 CHAVC 5  
|  
|  
|  
|  
|

## RESULT 29

US-10-105-008-95  
; Sequence 95, Application US/10105008  
; Publication No. US20030065136A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Ammar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401D1

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; CURRENT APPLICATION NUMBER: US/10/105,008
; CURRENT FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-105-008-95

Query Match          100.0%; Score 34; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
      |||||
Db      1 CHAVC 5

RESULT 30
US-10-425-557-81
; Sequence 81, Application US/10425557
; Publication No. US20040006011A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Ammar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shaomeng
; APPLICANT: Hu, Zhenjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.401C16
; CURRENT APPLICATION NUMBER: US/10/425,557
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-425-557-81

Query Match          100.0%; Score 34; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
      |||||
Db      1 CHAVC 5

RESULT 31
US-10-425-557-84
; Sequence 84, Application US/10425557
; Publication No. US20040006011A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Ammar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shaomeng
; APPLICANT: Hu, Zhenjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.401C16
; CURRENT APPLICATION NUMBER: US/10/425,557
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-425-557-84

Query Match          100.0%; Score 34; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
      |||||
Db      1 CHAVC 5

RESULT 32
US-10-425-557-85
; Sequence 85, Application US/10425557
; Publication No. US20040006011A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Ammar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shaomeng
; APPLICANT: Hu, Zhenjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.401C16
; CURRENT APPLICATION NUMBER: US/10/425,557
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-425-557-85

Query Match          100.0%; Score 34; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



```

; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-425-557-89

Query Match 100.0%; Score 34; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
   |||||
Db 1 CHAVC 5

RESULT 35
US-10-425-557-90
; Sequence 90, Application US/10425557
; Publication No. US2004006011A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shaomeng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.401C16
; CURRENT APPLICATION NUMBER: US/10/425,557
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-425-557-90

Query Match 100.0%; Score 34; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
   |||||
Db 1 CHAVC 5

RESULT 36
US-10-412-701-81
; Sequence 81, Application US/10412701
; Publication No. US20040058864A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shaomeng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION

```

```
; FILE REFERENCE: 100086.413C2
; CURRENT APPLICATION NUMBER: US/10/412,701
; CURRENT FILING DATE: 2003-04-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-412-701-81

Query Match          100.0%; Score 34; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      1 CHAVC 5
      |||||

RESULT 37
US-10-412-701-84
; Sequence 84, Application US/10412701
; Publication No. US20040058864A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.413C2
; CURRENT APPLICATION NUMBER: US/10/412,701
; CURRENT FILING DATE: 2003-04-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-412-701-84

Query Match          100.0%; Score 34; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      1 CHAVC 5
      |||||

RESULT 38
US-10-412-701-85
; Sequence 85, Application US/10412701
```

```
; Publication No. US20040058864A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.413C2
; CURRENT APPLICATION NUMBER: US/10/412,701
; CURRENT FILING DATE: 2003-04-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-412-701-85

Query Match          100.0%; Score 34; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      2 CHAVC 6
      |||||

RESULT 39
US-10-412-701-88
; Sequence 88, Application US/10412701
; Publication No. US20040058864A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.413C2
; CURRENT APPLICATION NUMBER: US/10/412,701
; CURRENT FILING DATE: 2003-04-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-412-701-88

Query Match          100.0%; Score 34; DB 15; Length 6;
```

Best Local Similarity 100.0%; Pred. No. 1.6e+06; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

Qy 1 CHAVC 5  
|||||  
Db 1 CHAVC 5

## RESULT 40

US-10-412-701-89  
; Sequence 89, Application US/10412701  
; Publication No. US20040058864A1  
; GENERAL INFORMATION:  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Ali, Anmar  
; APPLICANT: Ni, Feng  
; APPLICANT: Chen, Zhigang  
; APPLICANT: Michaud, Stephanie Denise  
; APPLICANT: Wang, Shoameng  
; APPLICANT: Hu, Zengjian  
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION  
; FILE REFERENCE: 100086.413C2  
; CURRENT APPLICATION NUMBER: US/10/412,701  
; CURRENT FILING DATE: 2003-04-19  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 89  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-10-412-701-89

Query Match 100.0%; Score 34; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||||  
Db 1 CHAVC 5

## RESULT 41

US-10-412-701-90  
; Sequence 90, Application US/10412701  
; Publication No. US20040058864A1  
; GENERAL INFORMATION:  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Ali, Anmar  
; APPLICANT: Ni, Feng  
; APPLICANT: Chen, Zhigang  
; APPLICANT: Michaud, Stephanie Denise  
; APPLICANT: Wang, Shoameng  
; APPLICANT: Hu, Zengjian  
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION  
; FILE REFERENCE: 100086.413C2  
; CURRENT APPLICATION NUMBER: US/10/412,701  
; CURRENT FILING DATE: 2003-04-19  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 90  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-10-412-701-90

Query Match 100.0%; Score 34; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||||  
Db 1 CHAVC 5

## RESULT 42

US-10-632-678-84  
; Sequence 84, Application US/10632678  
; Publication No. US20040106545A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Anmar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401C18  
; CURRENT APPLICATION NUMBER: US/10/632,678  
; CURRENT FILING DATE: 2003-08-01  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 84  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-10-632-678-84

Query Match 100.0%; Score 34; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||||  
Db 1 CHAVC 5

## RESULT 43

US-10-632-678-87  
; Sequence 87, Application US/10632678  
; Publication No. US20040106545A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Anmar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401C18  
; CURRENT APPLICATION NUMBER: US/10/632,678  
; CURRENT FILING DATE: 2003-08-01  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 87

; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-10-632-678-87

Query Match 100.0%; Score 34; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
| | | |  
Db 1 CHAVC 5

RESULT 44  
US-10-632-678-88  
; Sequence 88, Application US/10632678  
; Publication No. US20040106545A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Anmar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401C18  
; CURRENT APPLICATION NUMBER: US/10/632,678  
; CURRENT FILING DATE: 2003-08-01  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 88  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-10-632-678-88

Query Match 100.0%; Score 34; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
| | | |  
Db 2 CHAVC 6

RESULT 45  
US-10-632-678-91  
; Sequence 91, Application US/10632678  
; Publication No. US20040106545A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Anmar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401C18  
; CURRENT APPLICATION NUMBER: US/10/632,678  
; CURRENT FILING DATE: 2003-08-01

; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 91  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-10-632-678-91

Query Match 100.0%; Score 34; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
| | | |  
Db 1 CHAVC 5

RESULT 46  
US-10-632-678-92  
; Sequence 92, Application US/10632678  
; Publication No. US20040106545A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Anmar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 100086.401C18  
; CURRENT APPLICATION NUMBER: US/10/632,678  
; CURRENT FILING DATE: 2003-08-01  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 92  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-10-632-678-92

Query Match 100.0%; Score 34; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
| | | |  
Db 1 CHAVC 5

RESULT 47  
US-10-632-678-93  
; Sequence 93, Application US/10632678  
; Publication No. US20040106545A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Anmar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION

```
; FILE REFERENCE: 100086.401C18
; CURRENT APPLICATION NUMBER: US/10/632.678
; CURRENT FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
; US-10-632-678-93

Query Match      100.0%; Score 34; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
      |||||
Db      1 CHAVC 5

RESULT 48
US-10-632-678-100
; Sequence 100, Application US/10632678
; Publication No. US20040106545A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C18
; CURRENT APPLICATION NUMBER: US/10/632.678
; CURRENT FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 100
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
; US-10-632-678-100

Query Match      100.0%; Score 34; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
      |||||
Db      2 CHAVC 6

RESULT 49
US-09-769-145-86
; Sequence 86, Application US/09769145
; Patent No. US20020168761A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
```

```
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.413C1
; CURRENT APPLICATION NUMBER: US/09/769.145
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 09/491,078
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
; US-09-769-145-86

Query Match      100.0%; Score 34; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
      |||||
Db      1 CHAVC 5

RESULT 50
US-09-769-145-87
; Sequence 87, Application US/09769145
; Patent No. US20020168761A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.413C1
; CURRENT APPLICATION NUMBER: US/09/769.145
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 09/491,078
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
; US-09-769-145-87

Query Match      100.0%; Score 34; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-10-425-557-87

Query Match 100.0%; Score 34; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||  
Db 2 CHAVC 6

## RESULT 55

US-10-412-701-86  
; Sequence 86, Application US/10412701  
; Publication No. US2004005864A1  
; GENERAL INFORMATION:  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Ali, Annmar  
; APPLICANT: Ni, Feng  
; APPLICANT: Chen, Zhigang  
; APPLICANT: Michaud, Stephanie Denise  
; APPLICANT: Wang, Shoameng  
; APPLICANT: Hu, Zengjian  
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION  
; FILE REFERENCE: 10086.413C2  
; CURRENT APPLICATION NUMBER: US/10/412,701  
; CURRENT FILING DATE: 2003-04-19  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 86  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-10-412-701-86

Query Match 100.0%; Score 34; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||  
Db 1 CHAVC 5

## RESULT 56

US-10-412-701-87  
; Sequence 87, Application US/10412701  
; Publication No. US2004005864A1  
; GENERAL INFORMATION:  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Ali, Annmar  
; APPLICANT: Ni, Feng  
; APPLICANT: Chen, Zhigang  
; APPLICANT: Michaud, Stephanie Denise  
; APPLICANT: Wang, Shoameng  
; APPLICANT: Hu, Zengjian

; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION  
; FILE REFERENCE: 10086.413C2  
; CURRENT APPLICATION NUMBER: US/10/412,701  
; CURRENT FILING DATE: 2003-04-19  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 87  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-10-412-701-87

Query Match 100.0%; Score 34; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||  
Db 2 CHAVC 6

## RESULT 57

US-10-632-678-89  
; Sequence 89, Application US/10632678  
; Publication No. US20040106545A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; APPLICANT: Farookhi, Riaz  
; APPLICANT: Ali, Annmar  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION  
; FILE REFERENCE: 10086.401C18  
; CURRENT APPLICATION NUMBER: US/10/632,678  
; CURRENT FILING DATE: 2003-08-01  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 89  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide  
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal  
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group  
; OTHER INFORMATION: and/or C-terminal modifications such as amide or  
; OTHER INFORMATION: ester group  
US-10-632-678-89

Query Match 100.0%; Score 34; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||  
Db 1 CHAVC 5

## RESULT 58

US-10-632-678-90  
; Sequence 90, Application US/10632678  
; Publication No. US20040106545A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.

```
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Annar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C18
; CURRENT APPLICATION NUMBER: US/10/632,678
; CURRENT FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-632-678-90
Query Match 100.0%; Score 34; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 2 CHAVC 6

RESULT 59
US-10-632-678-96
; Sequence 96, Application US/10632678
; Publication No. US20040106545A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Annar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C18
; CURRENT APPLICATION NUMBER: US/10/632,678
; CURRENT FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 96
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-632-678-96
Query Match 100.0%; Score 34; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 3 CHAVC 7

RESULT 60
US-10-632-678-95
; Sequence 95, Application US/10632678
```

```
; Publication No. US20040106545A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Annar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C18
; CURRENT APPLICATION NUMBER: US/10/632,678
; CURRENT FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-632-678-95
Query Match 100.0%; Score 34; DB 16; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 3 CHAVC 7

RESULT 61
US-10-632-678-101
; Sequence 101, Application US/10632678
; Publication No. US20040106545A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Annar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C18
; CURRENT APPLICATION NUMBER: US/10/632,678
; CURRENT FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
; NAME/KEY: MOD_RES
; LOCATION: (5)
; OTHER INFORMATION: Where Xaa is beta,beta-dimethyl cysteine
US-10-632-678-101
Query Match 100.0%; Score 34; DB 16; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
```



```
Db          |||||
            3 CHAVC 7

RESULT 62
US-10-424-599-172220
; Sequence 172220, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 172220
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_126531C.1.pep
US-10-424-599-172220

Query Match      100.0%; Score 34; DB 15; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
        |||||
Db      30 CHAVC 34

RESULT 63
US-10-437-963-133433
; Sequence 133433, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 133433
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_35303C.1.pep
US-10-437-963-133433

Query Match      100.0%; Score 34; DB 16; Length 62;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
        |||||
Db      42 CHAVC 46

RESULT 64
US-10-425-115-323830
; Sequence 323830, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 323830
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_58402C.1.pep
US-10-425-115-323830

Query Match      100.0%; Score 34; DB 16; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
        |||||
Db      23 CHAVC 27

RESULT 65
US-10-291-172-630
; Sequence 630, Application US/10291172
; Publication No. US20030228584A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20030228584A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/291,172
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 630
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-172-630

Query Match      100.0%; Score 34; DB 15; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
        |||||
Db      61 CHAVC 65

RESULT 66
US-10-221-278-630
; Sequence 630, Application US/10221278
; Publication No. US20040034208A1
```

; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: No. US20040034208A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-045  
; CURRENT APPLICATION NUMBER: US/10/221,278  
; PRIOR FILING DATE: 2002-09-06  
; CURRENT FILING DATE: 09/693,267  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 09/665,363  
; PRIOR FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: 09/616,847  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 09/596,193  
; PRIOR FILING DATE: 2000-06-17  
; PRIOR APPLICATION NUMBER: 09/574,454  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: 09/519,705  
; PRIOR FILING DATE: 2000-03-07  
; NUMBER OF SEQ ID NOS: 752  
; SEQ ID NO 630  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-221-278-630

Query Match 100.0%; Score 34; DB 15; Length 121;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
|||||  
Db 61 CHAVC 65

## RESULT 67

US-10-437-963-196854  
; Sequence 196854, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 196854  
; LENGTH: 210  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_92667C.1.pep  
US-10-437-963-196854

Query Match 100.0%; Score 34; DB 16; Length 210;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
|||||  
Db 113 CHAVC 117

## RESULT 68

US-10-003-806-8  
; Sequence 8, Application US/10003806

; Publication No. US20020119929A1  
; GENERAL INFORMATION:  
; APPLICANT: Bishop, Colin E.  
; APPLICANT: Agoulnik, Alexander I.  
; APPLICANT: Zhu, Qichao  
; TITLE OF INVENTION: CAN 1 AND ITS ROLE IN MAMMALIAN INFERTILITY  
; FILE REFERENCE: P02066US1/10024824  
; CURRENT APPLICATION NUMBER: US/10/003,806  
; CURRENT FILING DATE: 2001-11-02  
; PRIOR APPLICATION NUMBER: 60/245,872  
; PRIOR FILING DATE: 2000-11-03  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 380  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-10-003-806-8

Query Match 100.0%; Score 34; DB 13; Length 380;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
|||||  
Db 318 CHAVC 322

## RESULT 69

US-10-437-963-137415  
; Sequence 137415, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 137415  
; LENGTH: 382  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_38900C.1.pep  
US-10-437-963-137415

Query Match 100.0%; Score 34; DB 16; Length 382;  
Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
|||||  
Db 36 CHAVC 40

## RESULT 70

US-10-437-963-151715  
; Sequence 151715, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 151715  
; LENGTH: 424  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_51834C.1.pep  
US-10-437-963-151715

Query Match 100.0%; Score 34; DB 16; Length 424;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
Db 39 CHAVC 43

RESULT 71  
US-10-437-963-197235  
; Sequence 197235, Application US/10417963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 197235  
; LENGTH: 513  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_93010C.1.pep  
US-10-437-963-197235

Query Match 100.0%; Score 34; DB 16; Length 513;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
Db 190 CHAVC 194

RESULT 72  
US-10-047-542-74  
; Sequence 74, Application US/10047542  
; Publication No. US20020168367A1  
; GENERAL INFORMATION:  
; APPLICANT: LARRICK, JAMES W.  
; APPLICANT: WYCOFF, KEITH L.  
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL  
; FILE REFERENCE: 030905.0004.CIP1

; CURRENT APPLICATION NUMBER: US/10/047,542  
; CURRENT FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: PCT/US01/13932  
; PRIOR FILING DATE: 2001-04-28  
; PRIOR APPLICATION NUMBER: 60/200,298  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 74  
; LENGTH: 537  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-10-047-542-74

Query Match 100.0%; Score 34; DB 13; Length 537;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
Db 96 CHAVC 100

RESULT 73  
US-10-425-115-315958  
; Sequence 315958, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 315958  
; LENGTH: 76  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_51224C.1.pep  
US-10-425-115-315958

Query Match 97.1%; Score 33; DB 16; Length 76;  
Best Local Similarity 80.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
Db 55 CHAVC 59

RESULT 74  
US-10-425-115-191667  
; Sequence 191667, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 191667  
; LENGTH: 82  
; TYPE: PRT

; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_106382C.1.pep  
US-10-425-115-191667

Query Match 97.1%; Score 33; DB 16; Length 82;  
Best Local Similarity 80.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
Db 50 CHAIC 54

## RESULT 75

US-10-437-963-159565  
; Sequence 159565, Application US/10437963  
; Publication No. US20040123343A1

## GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 159565

; LENGTH: 102

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_5892C.1.pep

US-10-437-963-159565

Query Match 97.1%; Score 33; DB 16; Length 102;  
Best Local Similarity 80.0%; Pred. No. 4.2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
Db 48 CHAIC 52

## RESULT 76

US-10-424-599-167243  
; Sequence 167243, Application US/10424599  
; Publication No. US20040031072A1

## GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J

; APPLICANT: Kovalic, David K

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 167243

; LENGTH: 110

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(110)

; OTHER INFORMATION: unsure at all xaa locations

; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_122038C.1.pep  
US-10-424-599-167243

Query Match 97.1%; Score 33; DB 15; Length 110;  
Best Local Similarity 80.0%; Pred. No. 4.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
Db 83 CHAIC 87

## RESULT 77

US-10-424-599-233727  
; Sequence 233727, Application US/10424599  
; Publication No. US20040031072A1

## GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J

; APPLICANT: Kovalic, David K

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 233727

; LENGTH: 241

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_53080C.1.pep

US-10-424-599-233727

Query Match 97.1%; Score 33; DB 15; Length 241;  
Best Local Similarity 80.0%; Pred. No. 8.2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
Db 104 CHAIC 108

## RESULT 78

US-10-424-599-276468  
; Sequence 276468, Application US/10424599  
; Publication No. US20040031072A1

## GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J

; APPLICANT: Kovalic, David K

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 276468

; LENGTH: 242

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_91670C.1.pep

US-10-424-599-276468

Query Match 97.1%; Score 33; DB 15; Length 242;  
Best Local Similarity 80.0%; Pred. No. 8.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5

Db 104 CHAIC 108  
|||:|

## RESULT 79

US-10-424-599-233725  
; Sequence 233725, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 233725  
; LENGTH: 243  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_53079C.1.pep  
US-10-424-599-233725

Query Match 97.1%; Score 33; DB 15; Length 243;  
Best Local Similarity 80.0%; Pred. No. 8.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
|||:|  
Db 106 CHAIC 110

## RESULT 80

US-10-437-963-178188  
; Sequence 178188, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 178188  
; LENGTH: 280  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_75769C.1.pep  
US-10-437-963-178188

Query Match 97.1%; Score 33; DB 16; Length 280;  
Best Local Similarity 80.0%; Pred. No. 9.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5  
|||:|  
Db 217 CHAIC 221

## RESULT 81

US-10-437-963-190970

; Sequence 190970, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 190970

; LENGTH: 343

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_87333C.1.pep

US-10-437-963-190970

Query Match 97.1%; Score 33; DB 16; Length 343;

Best Local Similarity 80.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5

|||:|

Db 126 CHAIC 130

RESULT 83

US-10-437-963-190972

; Sequence 190972, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 190970

; LENGTH: 343

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_87333C.1.pep

US-10-437-963-190970

Query Match 97.1%; Score 33; DB 16; Length 343;

Best Local Similarity 80.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5

|||:|

Db 126 CHAIC 130

RESULT 83

US-10-437-963-190972

; Sequence 190972, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 190970

; LENGTH: 343

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_87333C.1.pep

US-10-437-963-190970

Query Match 97.1%; Score 33; DB 16; Length 343;

Best Local Similarity 80.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5

|||:|

Db 126 CHAIC 130

RESULT 83

US-10-437-963-190972

; Sequence 190972, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 190970

; LENGTH: 343

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_87333C.1.pep

US-10-437-963-190970

Query Match 97.1%; Score 33; DB 16; Length 343;

Best Local Similarity 80.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5

|||:|

Db 126 CHAIC 130

RESULT 83

US-10-437-963-190972

; Sequence 190972, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 190970

; LENGTH: 343

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_87333C.1.pep

US-10-437-963-190970

Query Match 97.1%; Score 33; DB 16; Length 343;

Best Local Similarity 80.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5

|||:|

Db 126 CHAIC 130

RESULT 83

US-10-437-963-190972

; Sequence 190972, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 190970

; LENGTH: 343

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_87333C.1.pep

US-10-437-963-190970

Query Match 97.1%; Score 33; DB 16; Length 343;

Best Local Similarity 80.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5

|||:|

Db 126 CHAIC 130

RESULT 83

US-10-437-963-190972

; Sequence 190972, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 190970

; LENGTH: 343

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_87333C.1.pep

US-10-437-963-190970

Query Match 97.1%; Score 33; DB 16; Length 343;

Best Local Similarity 80.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5

|||:|

Db 126 CHAIC 130

RESULT 83

US-10-437-963-190972

; Sequence 190972, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 190972  
; LENGTH: 426  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_87335C.1.pap  
US-10-437-963-190972

Query Match 97.1%; Score 33; DB 16; Length 426;  
Best Local Similarity 80.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||:|  
Db 184 CHAIC 188

RESULT 84  
US-10-437-963-122755  
; Sequence 122755, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 122755  
; LENGTH: 728  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(728)  
; OTHER INFORMATION: unsure at all xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_25654C.1.pap  
US-10-437-963-122755

Query Match 97.1%; Score 33; DB 16; Length 728;  
Best Local Similarity 80.0%; Pred. No. 2e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||:|  
Db 310 CHAIC 314

RESULT 85

US-10-437-963-169219  
; Sequence 169219, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 169219  
; LENGTH: 777  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_6765C.1.pap  
US-10-437-963-169219

Query Match 97.1%; Score 33; DB 16; Length 777;  
Best Local Similarity 80.0%; Pred. No. 2.1e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||:|  
Db 590 CHAIC 594

RESULT 86  
US-10-437-963-201319  
; Sequence 201319, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 201319  
; LENGTH: 892  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_96706C.1.pap  
US-10-437-963-201319

Query Match 97.1%; Score 33; DB 16; Length 892;  
Best Local Similarity 80.0%; Pred. No. 2.3e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||:|  
Db 657 CHAIC 661

RESULT 87  
US-10-437-963-197899

; Sequence 197899, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 197899  
; LENGTH: 913  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_93612C.1.pep  
; US-10-437-963-197899

Query Match 97.1%; Score 33; DB 16; Length 913;  
Best Local Similarity 80.0%; Pred. No. 2.4e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||:|  
Db 682 CHAIC 686

RESULT 88

US-10-437-963-188555  
; Sequence 188555, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 188555  
; LENGTH: 946  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_85148C.1.pep  
; US-10-437-963-188555

Query Match 97.1%; Score 33; DB 16; Length 946;  
Best Local Similarity 80.0%; Pred. No. 2.4e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||:|  
Db 686 CHAIC 690

RESULT 89

US-10-629-313-146  
; Sequence 146, Application US/10629313

; Publication No. US20040176572A1  
; GENERAL INFORMATION:  
; APPLICANT: Nelson B. Freimer  
; APPLICANT: Hong Chen  
; APPLICANT: Victor I. Reus  
; APPLICANT: Susan K. Service  
; APPLICANT: Lynne Alison McInnes  
; APPLICANT: Pedro Leon  
; APPLICANT: Lodewijk Sandkuijl  
; TITLE OF INVENTION: Method and Compositions for Diagnosing and Treating Chromosome-18  
; TITLE OF INVENTION: Related Disorders  
; FILE REFERENCE: UCAL-154CIP5  
; CURRENT APPLICATION NUMBER: US/10/629,313  
; CURRENT FILING DATE: 2003-07-28  
; PRIOR APPLICATION NUMBER: 09/722,544  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 09/631,275  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: 09/268,992  
; PRIOR FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 09/236,134  
; PRIOR FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: 60/078,044  
; PRIOR FILING DATE: 1998-03-16  
; PRIOR APPLICATION NUMBER: 60/088,312  
; PRIOR FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/106,056  
; PRIOR FILING DATE: 1998-10-28  
; NUMBER OF SEQ ID NOS: 165  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 146  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-629-313-146

Query Match 91.2%; Score 31; DB 16; Length 18;  
Best Local Similarity 80.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5  
|||:|  
Db 9 CHAIC 13

RESULT 90

US-10-629-313-150  
; Sequence 150, Application US/10629313  
; Publication No. US20040176572A1  
; GENERAL INFORMATION:  
; APPLICANT: Nelson B. Freimer  
; APPLICANT: Hong Chen  
; APPLICANT: Victor I. Reus  
; APPLICANT: Susan K. Service  
; APPLICANT: Lynne Alison McInnes  
; APPLICANT: Pedro Leon  
; APPLICANT: Lodewijk Sandkuijl  
; TITLE OF INVENTION: Method and Compositions for Diagnosing and Treating Chromosome-18  
; TITLE OF INVENTION: Related Disorders  
; FILE REFERENCE: UCAL-154CIP5  
; CURRENT APPLICATION NUMBER: US/10/629,313  
; CURRENT FILING DATE: 2003-07-28  
; PRIOR APPLICATION NUMBER: 09/722,544  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 09/631,275  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: 09/268,992  
; PRIOR FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 09/236,134  
; PRIOR FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: 60/078,044  
; PRIOR FILING DATE: 1998-03-16  
; PRIOR APPLICATION NUMBER: 60/088,312

```
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/106,056
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-629-313-150

Query Match          91.2%; Score 31; DB 16; Length 18;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 9 CHALC 13

RESULT 91
US-09-864-761-35523
; Sequence 35523, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David K.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aomic-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35523
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; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000512.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.89
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EST_HUMAN HIT: AI281313.1, EVALUAE 5.00e-06
US-09-864-761-35523

Query Match          91.2%; Score 31; DB 9; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 1 CHALC 5

RESULT 92
US-10-437-963-174571
; Sequence 174571, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 174571
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_72499C.1.pap
US-10-437-963-174571

Query Match          91.2%; Score 31; DB 16; Length 49;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 21 CHSVC 25

RESULT 93
US-10-425-115-211467
; Sequence 211467, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
```



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; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 211467
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_124455C.1.pep
US-10-425-115-211467

Query Match          91.2%; Score 31; DB 16; Length 51;
Best Local Similarity 80.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 12 CHSVC 16

RESULT 94
US-10-424-599-163830
; Sequence 163830, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 163830
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_118958C.1.pep
US-10-424-599-163830

Query Match          91.2%; Score 31; DB 15; Length 55;
Best Local Similarity 80.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 50 CHALC 54

RESULT 95
US-09-864-761-34873
; Sequence 34873, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
```

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; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34873
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007695.12
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 21
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 7.4
; OTHER INFORMATION: SWISSPROT HIT: P34826, EVALUATE 9.00e-22
; OTHER INFORMATION: EST_HUMAN HIT: BE729465.1, EVALUATE 4.00e-23
US-09-864-761-34873

Query Match          91.2%; Score 31; DB 9; Length 63;
Best Local Similarity 80.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 36 CHALC 40

RESULT 96
US-10-424-599-190876
; Sequence 190876, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 190876
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: unsure at all xaa locations
; OTHER INFORMATION: Clone ID: MRT4577_115648C.1.pap
US-10-425-115-201825

Query Match          91.2%; Score 31; DB 15; Length 67;
Best Local Similarity 80.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      52 CHSVC 56

RESULT 97
US-10-291-265-762
; Sequence 762, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR FILING DATE: 2000-01-25
; PRIOR FILING DATE: 2000-07-17
; PRIOR FILING DATE: 2000-07-17
; PRIOR FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-09-15
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 762
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-762

Query Match          91.2%; Score 31; DB 15; Length 96;
Best Local Similarity 80.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      81 CHSVC 85

RESULT 98
US-10-425-115-201825
; Sequence 201825, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 201825

; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 183087
; LENGTH: 100

RESULT 100
US-10-424-599-183087
; Sequence 183087, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 183087
; LENGTH: 100

; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 118366
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_21685C.1.pap
US-10-437-963-118366

Query Match          91.2%; Score 31; DB 16; Length 98;
Best Local Similarity 80.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      75 CHAMC 79

RESULT 99
US-10-437-963-118366
; Sequence 118366, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 118366
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_21685C.1.pap
US-10-437-963-118366

Query Match          91.2%; Score 31; DB 16; Length 98;
Best Local Similarity 80.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      75 CHAMC 79

RESULT 100
US-10-424-599-183087
; Sequence 183087, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 183087
; LENGTH: 100
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; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_136340C.1.pep
US-10-424-599-183087

Query Match      91.2%; Score 31; DB 15; Length 100;
Best Local Similarity 80.0%; Pred. NO. 8.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      1 CHAVC 5
        ||:|
Db      96 CHSVC 100
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Search completed: July 27, 2005, 00:14:44  
Job time : 159 secs

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